


```

Qy 135 SEVVKLSSEKNAKEINVHGRLEKLNLYNMANIENYVDSKVANLTFVYNSLDGKSCX 194
Dy 160 NLDNIPSSLRVLRVIDSLHKKIQKL-----EVAATQ-----DYCESPC 201
Qy 195 PSQGIQSRPQVHLYKDCDYAIGKBSSEYRVTPDKNSSEFYVCDYETNGGWTVL 254
Db 202 -----VASCI:PVVSGRECEIDYRKGETSEMIIQDPPT--PYRYVCDYETNGGWTJ 256
Qy 255 QARLDGSGTNEFRWCQYKAGFGNLR-----EFLWGNCKIHLITKSKMELRID 303
Db 257 QNRGGVWFGRAWDEYKRGFGNIAKGGKCYDTPGEYWLGNCKISQJTKIGPTKVLJE 316
Qy 304 LEDNGVHLYALYDCFYVANEFLKYRLHVNNGTAGDALR--FNKSKY-----HDK 354
Db 317 MEDWNGKVSALYGGPTIHNEGKYQSVNGYKGNAGNALYEGASQLYGENRTMTTHNG 376
Qy 355 FFTPTPKDNRY----PSGNCGLYSSGWFACLSANLNGKY-----HKKYRGVFN 403
Db 377 YFSYDRNDGHLTTPRKQSGEDGGWYNNRCHANPNRYNGSTYSWDAKAGTDD 436
Qy 404 GIFMGTPGVSEAHPGGYKSFKEAKMIRP 434
Db 437 GIVWAKKG-----SWY--SMKMSMKIRP 459

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RESULT 5

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fibrinogen-related protein HFRP-1 precursor - human
C:Species: Homo sapiens (man)
C>Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 21-Jul-2000
C:Accession: U00596
R:Yamamoto, T.; Gotoh, M.; Sasaki, H.; Terada, M.; Kitajima, M.; Hirohashi, S.
Biochem. Biophys. Res. Commun. 193, 681-687, 1993
A:Title: Molecular cloning and initial characterization of a novel fibrinogen-related
A:Reference number: U00596; MUID:93290661; PMID:8390249
A:Accession: U00596
A:Molecule type: mRNA
A:Residues: 1-312 <YAM>
A:Cross-references: GB:D:4446; NID:G393314; PIDN:BAAG3336.1; PID:G393315
A:Experimental source: liver
C:Superfamily: fibrinogen beta/gamma homology
F:1-17/Domain: signal sequence #status predicted <SIG>
F:18-312/Product: fibrinogen-related protein HFRP-1 #status predicted <MAT>
F:80-305/Domain: fibrinogen beta/gamma homology <FBG>

```

```

Query Match 21.38; Score 506.5; DB 2: Length 312;
Best Local Similarity 36.88; Pred No. 1e-27;
Matches 118; Conservative 38; Mismatches 106; Indels 57; Gaps 3;

Qy 129 RVRELESEVKNLSSELYKNAKEINVHGRLEKLNLYNMANIENYVDSKVANLTFVYNSLD 188
Db 36 QVRLLETRVKQQVKIKQLLQF-----NEVQFLKGGDEDTWJ----- 73
Qy 199 GKCSKCPSEQIQSRPVQHLYKDCSDYYA:GKSSSEYRVTPDKNSSEFYVCDYETNG 248
Db 74 -----LGSKRO-----YACSEIFNDGKLSGYKIKELQSPAFSFCVDCXSG-G 117
Qy 249 GGWTVQARLDGSGTNRFTWCYKAGFGNL---RRFELNGNCKIHLITKSKMELRIDE 305
Db 118 GGWTVIQERSDGSSENFNRGNKDYENGFGNFVQKGEVWJGNKNHFLTCEDYTLKIDLA 177
Qy 306 DFNQGVLYALYDQFYVANEFLKYRLHVNNGTAGDALRNGK-----YNHDLKFFTP 359
Db 178 DFENKSRVAOYKFNKVGDEKNFYEJNTEYSGTAGDSLACNPFPEVQWASHQRMKFE 217
Qy 360 DKDNDYRPSGNCGLYSSGWFACLSANLNGKYHGXKYG-VRNGIPACTGVGVSEAH 418
Db 239 DRDHNY-EGNCAEEDSGGWNFNCHSANLNGVYSGPYAKTDNGVWYTW----- 288
Qy 419 GGYKSSFKFAKQM:RPKHFKP 439
Db 289 HGWYLSKSVNKKRPNDPFP 309

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RESULT 6

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fibrinogen gamma-B chain precursor (validated); - human
N:Alternate names: coagulation factor I; fibrinogen gamma-55 chain
C:Species: Homo sapiens (man)
C>Date: 17-Mar-1987 #sequence_revision 17-Mar-1987 #text_change 08-Dec-2000
C:Accession: A90494; A92448; A90453; A28203; B28203; I37390; A63126
R:Prixon, M.W.; Chung, D.W.; Davie, E.W.
Biochemistry 24, 2077-2086, 1985
A:Title: Nucleotide sequence of the gene for the gamma chain of human fibrinogen.
A:Reference number: A90494; MUID:85252774; PMID:2593550
A:Accession: A93494
A:Molecule type: DNA
A:Residues: 1-113, 115-453 <RIX>
A:Cross-references: GB:M10014; GB:J00134; GB:J00135; GB:X00086; NID:G182438; PIDN:AAB5
R:Forace Jr., A.C.; Cummings, D.E.; Comeau, C.M.; Kant, J.A.; Crattree, G.R.
J. Biol. Chem. 259, 12826-12830, 1984
A:Title: Structure of the human gamma-fibrinogen gene. Alternate mRNA splicing near th
A:Reference number: A92448; MUID:85030379; PMID:6092346
A:Accession: A92448
A:Molecule type: DNA
A:Residues: 286-453 <FOR>
R:Wolfenstein-Todel, C.; Meselson, M.W.
Biochemistry 20, 6146-6149, 1981
A:Title: Carboxy-terminal amino acid sequence of a human fibrinogen gamma-chain varian
A:Reference number: A90453; MUID:82068993; PMID:7306501
A:Accession: A90453
A:Molecule type: protein
A:Residues: 411-434, 436-440, 442, 444, 446-447, 449, 453 <WOL>
R:Francis, C.W.; Mueller, E.; Henschen, A.; Simpson, P.J.; Marder, V.J.
Proc. Natl. Acad. Sci. U.S.A. 85, 3358-3362, 1988
A:Title: Carboxy-terminal amino acid sequences of two variant forms of the gamma-chai
A:Reference number: A94194; MUID:86217900; PMID:3368448
A:Accession: A28203
A:Molecule type: protein
A:Residues: 433-449 <FRA>
A:Accession: B28203
A:Molecule type: protein
A:Residues: 433-453 <FR2>
R:Marchetti, L.; Zanelli, T.; Malcovati, M.; Turchini, M.L.
DNA Seq. 1, 419-422, 1991
A:Title: Polymorphism of the human gamma chain fibrinogen gene.
A:Reference number: I37390; MUID:92119334; PMID:1685103
A:Accession: I37390
A:Status: translated from GS/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 73-286 <RES>
A:Cross-references: EMBL:X51473; NID:G31410; PIDN:CAA35837.1; PDI:9930064
C:Comment: The two forms of gamma chain, A (see PIR:FGHUG) and B, arise by alternate s
tron, which makes this chain different from the gamma-B chain at positions 434-437 an
C:Comment: The gamma-B chain is present in about 10% of the fibrinogen molecules in pi
C:Genetics:
A:Gene: GDB:FGG
A:Cross-references: GDB:I19132; OMIM:134850
A:Map position: 4q28-4q28
A:Coordinates: 26/3; 41/3; 103/1; 134/2; 178/1; 222/3; 284/2; 377/1
C:Complex: The fibrinogen molecule is a hexamer containing two sets of alpha (see PIR:
has are contained in the core. Two three-chain coiled coils emerge from this core and
from the distal domain nodes.
C:Function:
A:Description: fibrinogen cleaved by thrombin yields monomers that are polymerized int
A:Pathway: blood coagulation
C:Superfamily: fibrinogen gamma chain; fibrinogen beta/gamma homology
C:Keywords: alternative splicing; blood coagulation; calcium; coiled coil; glycoprotei
F:1-26/Domain: signal sequence #status predicted <SIG>
F:27-453/Product: fibrinogen gamma-B chain #status experimental <MPT>
F:176-415/Domain: fibrinogen beta/gamma homology <FBG>
F:341-355/Domain: calcium binding #status predicted <CAB>
F:400-422/Region: polymerization site, binding to the amino end of the alpha chain of
F:34/Disulfide bonds: interchain (to gamma-35) #status predicted
F:35/Disulfide bonds: interchain (to gamma-34) #status predicted
F:45/Disulfide bonds: interchain (to beta-110) #status predicted

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QY 259 DGSTNFRTRWDYKAGFGNLR-----REFWLGNDKIHLTKSKXEMILRDLSDFF 307
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 278 DGSNSFARDWNTYKAEFGNI:AFNGKSGICNIPOEYWLGTKTVHQLTKQTQQVFDMSDW 337

QY 306 NGVELVALIDOFYVANEFLKYRLHVGNYNAGTAGDAL-----RENKHYN-HDJKFTT 358
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 338 EGSVVTAQVASPFEAQAQGYRLWVEDYSNAGNAJLEGATQMCDNRRTMTIHNGKQFST 397

QY 359 PDKNDNRY----PSGNCGLYSSGMWFDACLSANLNGYY-----HKYEGVANG:FW 407
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 398 FDRDNWNPNPGDPTKHSREDACGMVNVRCHAAANPNRGVYWGGIYTKAQDYGTDDGVVW 457

QY 406 GTWPGVSEAHPPGGYKSFKFAKMIRPK 435
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 458 MNWKG-----SWY--SYRMAMKLIRPK 477

RESULT 9
FGBOB
N:Contains: fibrinopeptide B
C:Species: Bos primigenius taurus (cattle)
C>Date: 29-Jul-1981 #sequence, revision 29-Jul-1981 #text_change 13-Sep-1996
C:Accession: A03122; R03117; B37507; A37513; S02443
R:Blomback, B.; Doolittle, R.F.
Acta Chem. Scand. 17, 1916-1919, 1963
A>Title: The sequence of amino acids at the N-terminal end of bovine fibrinopeptide B.
A:Reference number: A03122
A:Accession: A03122
A:Molecule type: protein
A:Residues: 1-4 <BLO>
R:Sjoquist, J.; Blomback, B.; Wallen, P.
Ark. Kemi 16, 425-436, 1960
A>Title: Amino acid sequence of bovine fibrinopeptides.
A:Reference number: A03117
A:Accession: B03117
A:Molecule type: protein
A:Residues: 5-21 <SJO>
R:Martinelli, R.A.; Inglis, A.S.; Rubira, M.R.; Hageman, T.C.; Rutrell, J.G.R.; Leach, S.
Arch. Biochem. Biophys. 192, 27-32, 1979
A>Title: Amino acid sequences of portions of the alpha and beta chains of bovine fibrin
A:Reference number: A37507; MJJD:79164394; PMID:434821
A:Accession: B37507
A:Molecule type: protein
A:Residues: 22-53 <MAR>
R:Chung, D.W.; Rixson, M.W.; MacGillivray, R.T.A.; Davie, E.W.
Proc. Natl. Acad. Sci. U.S.A. 78, 1466-1470, 1981
A>Title: Characterization of a cDNA clone coding for the beta chain of bovine fibrinogen
A:Reference number: A37513; MCB:D:81199473; PMID:6262803
A:Accession: A37513
A:Molecule type: mRNA
A:Residues: 44-468 <CHU>
R:Medved, L.V.; Platonova, T.N.; Litvinovich, S.V.; Lukinova, N.I.
FEBS Lett. 232, 56-60, 1988
A>Title: The cleavage of beta-chain in bovine fibrinogen D(H) fragment (95 kDa) leads to
A:Reference number: S02443; MCB:D:88211875; PMID:2966748
A:Accession: S02443
A:Molecule type: protein
A:Residues: 373-374 <MED>
C:Comment: Thrombin cleaves the bond between Arg-21 and Gly-22 to release fibrinopeptide
C:Comment: Fibrinogen is a hexamer containing two sets of three nonidentical chains (alpha
C:Superfamily: fibrinogen beta chain: fibrinogen beta/gamma homology; fibrinogen disulfide
C:Keywords: blood coagulation; glycoprotein; plasma; pyroglutamic acid; sulfoprotein
P:76-205/Domain: fibrinogen disulfide ring homology <FBG>
P:215-464/Domain: fibrinogen beta/gamma homology <FBG>
P:1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
P:6/Binding site: sulfate (Tyr) (covalent) #status experimental
P:21-22/Cleavage site: Arg-gly (thrombin) #status experimental
P:371/Binding site: carbonylate (Asn) (covalent) #status experimental
P:372-373/Cleavage site: Arg-Thr (plasmin) #status experimental

Query Match 19.8% Score 470; DB 1; Length 468;

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Best Local Similarity 30.6%; Pred. No. 5.8e-25;
Matches 129; Conservative 57; Mismatches 149; Indels 86; Gaps 13;

QY      61 LPPLTIQLPKPQSRIEE-VFKEVQNLAKEIVNSLKKSCQC--KLQADNDGDPGRNGLLLP 117
       ||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB      82 LCPTCKLQDLTVRQERPIKSIEDLRNTVDVSRTSSSTFOYTLLKNMKCR----- 135

QY     118 STGAPGEVDNRVRELESEVNKLSELKNAKEINVILHGLEKLNLYNNANIENYDSKV 177
       ||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB     136 -----QNVQDNEMVNEYSS-----HLEKHQLYIDETVKNIPTKL 172

QY     178 AKLTFTVNSLDGCKSKCPSQEQISR-----PVQHLTKDCSDVYAIGKRSE 225
       ||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB     173 RVLRSILENLASKIOLUESDVSTQMEYCRTPTCTVTICNPV--VSGKECEKIIRNEGTSE 230

QY     226 TVRVTPDKNKSFEVYCDMETMGGWKTVLQARLDGSTNFTRTWODYKAGRNLR----- 280
       ||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB     231 MYLIOPEDSSKPYYCDMKTCKGWTVIQNRDGSLDFGRKWDPYKQGFNIATNAEGK 290

QY     281 -----EFWLGNDRKHLLTTSKEMILRIDLEDENGVELVALYPQVFANEFKYRLHV 333
       ||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB     291 KYCGVPGEVWLGNDRIISQLTNMGPTKLLIENEDWKDGKVTALEYGVTFQEKANKYQLSVS 350

QY     334 NYNVTAGDAL-----RPNKHYN-HDLKFFTPDKNDRY-----PSGNCGLYYSSGW 380
       ||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB     351 KYKGAGNALIEGASQLGENRTITIHNSMFSTYDRDNCGMKTTDRKQCKSEDGGGW 410

QY     382 FPACLSANLNGKYY-----HQYRGVRNGIFWGTPGVSEAHPGGYKSFKAQMIR 433
       ||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB     411 YNECHANPEGYNGGAYTDMAKHGTTDDGVVMNWQG-----SWY--SMKKYSMKIR 462

QY     434 P 434
       |
DB     463 P 463

RESULT 10
SQ5313
C:fibrinogen gamma-B chain precursor - bovine
C:Species: Bos primigenius taurus [cattle]
C>Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 13-Aug-1999
C:Accession: SQ5313
R:Brown, W.M.; Dziewielewska, K.M.; Foreman, R.C.; Saunders, N.R.
Nucleic Acids Res. 17, 6397, 1989
A:title: Nucleotide and deduced amino acid sequence of a gamma subunit of bovine fibrin
A:Reference number: SQ5313; MUID:89366676; PMID:2771651
A:Accession: SQ5313
A:Molecule type: mRNA
A:Residues: 1-444 <PRO>
A:Cross-references: EMBL:X:5556; NID:9349; PIDN:CAA33562.1; P:D:Q350
A>Note: The authors translated the codon AGT for residue 105 as Ala and ATT for residue 106 as Asn.
C:Superfamily: fibrinogen gamma chain; fibrinogen beta/gamma homology
F:1-24/Domain: signal sequence #status predicted <SIG>
F:25-444/Product: fibrinogen gamma-B chain #status predicted <MAT>
F:174-414/Domain: fibrinogen beta/gamma homology <PB3>

Query Match          19.4%; Score 462; DB 2; Length 444;
Best Local Similarity 30.5%; Pred. No. 1.9e-24;
Matches 142; Conservative 51; Mismatches 164; Indels 108; Gaps 19;

QY      9 LSAVIAITYGFLVANNTEETIKBRACXVCPRV-ESRGKCEAGECPYQSLPPLTIQL 68
       ||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB     18 LSSACL-----YVATRONCCILDERFGSYCPT-----TCGIADFNNYQTSV 60

QY     69 PROFSRIEVFVEKONLEIVNSLKKSCODCKLOADDNDGDPGRNGLLLPSTGAPGEUCDN 128
       ||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB     61 DKDLRTLLEGILYQVENTKSEARELVKA-----IQISYNPDQ----- 96

QY    129 RVRELSEVNKLSELKNAK---EELNVLHGRLEKLNLYN-----MNINENYDSKV 177
       ||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB     97 -----PSKPNNISATIONSKMMEI-----MKYETLISTHESTIRLFQEVYNSOKI 145

QY   178 ANLFTVNSLDGCKSKCPSEQIQSRPVQHLYTKDCSDVYAIGKRSETYRTVFPKNSS 237

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Db      146 VNLKRVKVLKQVLEANCQF-PQDITVK---HDVTGRCDQVANKAKESGLYFIRP-LKAKQ 200
QY      238 FEVYCDVETMGQGTWTLQARLDGSGNFTRTWQDYKAGFGLN-----RREWLGNKXHL 291
Db      201 FLVYCEIDSGNGWTVFQKRLDGLSLDFKKNQIQYKRGFGHISPTGTGNTFELWGNFX-KHL 260
QY      292 LTKSKEM--ILRDLDFNGVHLYALYDQFYVANKELKYLKLVHGVHY-NGTAGDA----- 343
Db      261 ISTQSSIPVYLRQLEDMKGRSTADYASFKYTGENDKYLFLYAVFPGCAGDAGTGYDF 320
QY      344 ---RPNKHV-NMDLKEFTTDCNDNRYPSGNGGLYSSQWMTFACLSANLNSKYVH----- 395
Db      321 GDSSDKFTTSHNQFSTWSDNDXY-DGNCAGQVGIQWNNKXCHAGHLNSGVYTCGTY 379
QY      396 ---QKVGVRNGIFWTFQVSEAHFGGYKS---SPKEAKMMIRP 434
Db      380 SKTSTPNGYDNG-IWATW-----KSRWYSKKXTTKIIP 413

RESULT 11
FGHUB
N:Alternate names: coagulation factor 1
N:Contains: fibrinopeptide B
C:Species: Homo sapiens (man)
C:Date: 24-Apr-1984 #sequence, revision 31-Mar-1993 #text_change 08-Dec-2003
C:Accession: B43568; B90469; I37389; A94433; A90437; A94309; G54223; B3
R:Chung, D.W.; Harris, J.E.; Davie, E.W.
Adv. Exp. Med. Biol. 281, 39-48, 1990
A:Title: Nucleotide sequences of the three genes coding for human fibrinogen.
A:Reference number: A43568; MUID:9134474C; PMID:2102623
A:Accession: B43568
A:Molecule type: DNA
A:Residues: 9-191, 'P', 193-491 <CHU>
R:Chung, D.W.; Que, B.G.; Rixon, M.W.; Mace G.R., M.; Davie, E.W.
Biochemistry 22, 3244-3250, 1983
A:Title: Characterization of complementary deoxyribonucleic acid and genomic deoxyribonu
A:Reference number: A90469; MUID:83233433; PMID:6688356
A:Accession: A90469
A:Molecule type: DNA
A:Residues: 1-38 <CH>
A:Accession: B90469
A:Molecule type: mRNA
A:Residues: 9-191, 'A', 193-491 <CH2>
A:Cross-references: GB:J030229; NID:9182429; PIDN:AAAS2429.1; PDB:1G1R241C
R:Huber, P.; Dalmon, C.; Courtois, G.; Laurent, M.; Assouline, Z.; Marguerie, G.
Nucleic Acids Res. 15, 1615-1625, 1987
A:Title: Characterization of the 5'-flanking region for the human fibrinogen beta gene.
A:Reference number: I37389; MUID:97146483; PMID:3029722
A:Accession: I37389
A:Status: translated from GB/EXBL/DBJ
A:Molecule type: DNA
A:Residues: 1-38 <HUB>
A:Cross-references: EMBL:X05018; NID:931400; PIDN:CAAZ8674.1; PID:g31401
R:Henschen, A.; Lottspeich, F.; Southan, C.; Tzipori-Petersen, E.
in: Profiles of the Biological Fluids. Proc. 28th Colloq. Peeters, H., ed., pp.51-55, Pe
A:Title: Human fibrinogen: sequence, sulfur bridges, glycosylation and some structural v
A:Reference number: A94433
A:Contents: Carbohydrate binding
A:Accession: A94433
A:Molecule type: protein
A:Residues: 31-137, 'QS', 140-144, 'QF', 147-491 <HEN>
R:Watt, K.W.K.; Takagi, T.; Doolittle, R.F.
Biochemistry 18, 68-76, 1979
A:Title: Amino acid sequence of the beta chain of human fibrinogen.
A:Reference number: A90437; MUID:79124640; PMID:420779
A:Accession: A90437
A:Molecule type: protein
A:Residues: 31-144, 'QF', 147-231, 'D', 233-330, 'E', 332-491 <WAT>
R:Blomback, B.; Hessel, B.; Hogg, D.
Thromb. Res. 8, 639-658, 1976
A:Title: Disulfide bridges in NH-2-terminal part of human fibrinogen.

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A:Reference number: A94309; MUID:76225080; PMID:936108
A:Contents: disulfide bonds
A:Accession: A94309
A:Molecule type: protein
A:Residues: 31-112, 'E', 114-137, 'QS', 140-144, 'QF', 147-148 <BLO>
R:Xunitake, S.; Carilli, C.T.; Lau, K.; Protter, A.A.; Naya-Vigne, J.; Kane, J.P.
Biochemistry 33, 1988-1993, 1994
A:Title: Identification of proteins associated with apolipoprotein A-I-containing lipo
A:Reference number: A54223; MUID:94162201; PMID:8117655
A:Accession: G54223
A:Molecule type: protein
A:Residues: 164-174 <KM>
A:Note: Identification of tryptic peptides from high-density lipoproteins
R:Henschen, A.; Lottspeich, F.; Kehl, M.; Southan, C.
Ann. N. Y. Acad. Sci. 408, 28-43, 1983
A:Title: Covalent structure of fibrinogen.
A:Reference number: A90037; MUID:83254370; PMID:6575689
A:Contents: annotation; review, disulfide bonds
R:Gardlund, B.; Hessel, B.; Marguerie, G.; Murano, G.; Blomback, B.
Eur. J. Biochem. 77, 595-610, 1977
A:Title: Primary structure of human fibrinogen. Characterization of disulfide-containi
A:Reference number: A91249; MUID:77245999; PMID:891553
A:Contents: annotation; disulfide bonds
R:Doolittle, R.F.; Takagi, T.; Watt, K.; Bouma II, H.; Cottrell, B.A.; Cassman, K.G.;
in: Regulatory Proteolytic Enzymes and Their Inhibitors, Magnusson, S., Ottesen, M., Po
A:Title: The structures of fibrinogen and fibrin.
A:Reference number: A94437
A:Contents: annotation; disulfide bonds
R:Doolittle, R.F.
Annu. Rev. Biochem. 53, 195-229, 1984
A:Title: Fibrinogen and fibrin.
A:Reference number: A90041; MUID:84305751; PMID:6383194
A:Contents: annotation; review, EM structure, polymerization, ligands
R:Chung, D.W.; Rixon, M.W.; Que, B.G.; Davie, E.W.
Ann. N. Y. Acad. Sci. 408, 449-456, 1983
A:Title: Cloning of fibrinogen genes and their cDNA.
A:Reference number: A90038; MUID:83254384; PMID:6575700
A:Contents: annotation
R:Kirschbaum, N.E.; Budzynski, A.Z.
J. Biol. Chem. 265, 13669-13676, 1990
A:Title: A unique proteolytic fragment of human fibrinogen containing the Aalpha COOH-
A:Reference number: A37117; MUID:90337977; PMID:2143188
A:Contents: annotation; hementin cleavage site
A:Note: hementin, a protease from Haemophilia ghiliani, the giant South American leec
C:Comment: The conversion of fibrinogen to fibrin is triggered by thrombin, which clea
C:ation sites responsible for the formation of the soft clot.
C:Comment: The soft clot is converted into the hard clot by factor XIIIa (fibrin-stabi
ger) and between alpha chains (weaker) of different monomers.
C:Comment: All fibrinogen chains are synthesized in the liver.
C:Genetics:
A:Gene: GDB:FCB
A:Cross-references: GDB:119130; OMIM:134830
A:Map position: 4q28-q28
A:Introns: 38/3; 102/3; 164/1; 240/1; 278/1; 320/1; 415/2
C:Complex: The fibrinogen molecule is a hexamer containing two sets of alpha (see P.R:
is are contained in the core. Two three-chain coiled coils emerge from this core and
from the distal domain nodes.
C:Function:
A:Description: fibrinogen cleaved by thrombin yields monomers that are polymerized int
A:Pathway: blood coagulation
A:Superfamily: fibrinogen beta chain; fibrinogen beta/gamma homology; fibrinogen disul
C:Keywords: blood coagulation; coiled coil; glycoprotein; liver; plasma; pyroglyutamic
F.1-30/Domain: (or 4-30 or 15-30) signal sequence #status predicted <SIG>
F.31-491/Product: fibrinogen beta chain #status experimental <MAT>
F.31-44/Product: fibrinopeptide B #status experimental <API>
F.45-491/Product: fibrin beta chain #status experimental <API>
F.45-47/Region: polymerization site
F.99-228/Domain: fibrinogen disulfide ring homology <FDR>
F.238-487/Domain: fibrinogen beta/gamma homology <FBG>
F.31/Modified site: pyrrolidone carboxylic acid (Gln) (in mature form) #status experim
F.44-45/Cleavage site: Arg-Gly (thrombin) #status experimental
F.95/Disulfide bonds: interchain (to alpha-55) #status experimental
F.106/Disulfide bonds: interchain (to alpha-68) #status experimental

```

F:110/Disulfide bonds: interchain (to gamma-45) #status experimental
F:223/Disulfide bonds: interchain (to alpha-184) #status experimental
F:227/Disulfide bonds: interchain (to gamma-161) #status experimental
F:231-316,241-270,424-437/Disulfide bonds: #status experimental
F:394/Birding site: carbohydrate (asn) (covariant) #status experimental

Query Match 19.4%; Score 461; DB 1; Length 491;
Best Local Similarity 28.7%; Pred. No. 2.6e-24;
Matches 133; Conservative 57; Mismatches 161; Indels 112; Gaps 14;

QY 27 TEEIKDERAKVCPVRLSRGKCEAGE-----CPQVSLPELTQLPKQF-SRISEVEK 80
DB 81 TOKKVERKAPDA-----GGCUHAPDLGLVLCPTCCQQLQOEPIRNSVDLNN 132
QY 81 EVQNLKIVRS-----LKKSCQCKLQADKQDGPGRNGLLLESTGAPGEVDNRVRL 133
DB 133 NVEAVSQTSSSSFOYVYLLKDLQKQKQVKCN-----165
QY 134 ESEVNLKLSSELKNAKEINVLHGRLEKLNLMNNIENYVDSKVANLTFVNSLDKCSK 193
DB 166 ENNVNYSSE-----LEKHQYIDETVNSNPTLNLRLSILENLSKIQK 211
QY 194 CPSQEQIQ-----SRPVQHLIYKQSDYVAIGKRSESYRVTPPKRSSEFWYCD 243
DB 212 LESDVSQAQVEYCRTPCVSNKIPVUSCKECEE::RKGEISEYLIQPCSSVKPYRYCD 271
QY 244 METHGGGWTVLQARLDGSTNTRTWQDYKAGFN-----LRREFWLGNDKIHIL 291
DB 272 MNTENGKMTIQNRQSGVDFGRKMDPYKQGFQGNVATNTDKNYCGLPGEYWLJGNDKISQ 331
QY 292 LTKSKEMILRILEDENGVVELYALYDCQFYVANFLKYRLHVGNVNTAGDALR-----344
DB 332 LTRMGPTELLLEMDWKGDKVKAHYGGFTVQNEANKQISVNYKRGTAGNALWGSQSLN 391
QY 345 -FNKHYN-HDLKFTTPKXNDRY-----PSGNGLYVSSQWDFDACLSANLNGKYV-----394
DB 392 GENRTMTIHNGMPESTYDRDNGDLTDPKQCKSKEDGGGWYNRCHAAANPNRYWKGQ 451
QY 395 ---HQRVGRVNGIFWKTQGVSEAHFGGYKSFKEKAKKWRP 434
DB 452 YTWDMAXHGTDGCVVMNKKG-----SWY--SMRKMMSKIRP 466

RESULT 12
A:132670
fibrinogen gamma chain - African clawed frog
C:Species: Xenopus laevis (African clawed frog)
C:Date: 15-Jun-1990 #sequence_revision 15-Jun-1990 #text_change 13-Aug-1999
C:Accession: A32670; I51416
R:Pastori, R.L.; Moskaitis, J.E.; Smith Jr., L.H.; Schenber, D.R.
B:Biochemistry 29, 2599-2605, 1992
A:Title: Estrogen regulation of Xenopus laevis gamma-fibrinogen gene expression.
A:Reference number: A32670; NUID:90241882; PMID:2334684
A:Accession: A32670
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-438 <PAS>
A:Cross-references: GB:J02694; NID:G2:41339; PIDN:AAA49709.1; PID:G2:4140
R:Bhattacharya, A.; Shepard, A.R.; Moser, D.R.; Holland, L.G.
Mol. Cell. Endocrinol. 72, 213-220, 1990
A:Title: Isolation and characterization of cDNA clones for the gamma subunit of Xenopus
A:Reference number: I51416; MVID:9:146806; PMID:2289632
A:Accession: I51416
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-58 <BHA>
A:Cross-references: GB:M35548; NID:G2:4141; PIDN:AAA03247.1; PID:G2:4142
C:Superfamily: fibrinogen gamma chain; fibrinogen beta/gamma homology
C:Keywords: blood coagulation
F:173-413/Domain: fibrinogen beta/gamma homology <FEG>

Query Match 19.2%; Score 456; DB 2; Length 438;
Best Local Similarity 30.4%; Pred. No. 5e-24;

Matches 130; Conservative 69; Mismatches 158; Indels 70; Gaps 17;
QY 10 SSAYLATYGVGLVANNETEBIKDERAKDVCPVRLSRGKCEAGECPYQVSLPELTQLP 69
DB 14 SLALLSAGFNIPNTDNCILDRGEYCF-----TCG:5 50
QY 70 KQFSRIEE-VFKEVQNLKEIVNSLKKSCQCKLQADNDGDPGRNGLLLESTGAPGEVGN 128
DB 51 DFLNRYQENVDTQLYLENLLTQISNSTSGTTIIVEHLIDSGKKPATSPQATL-----DF 105
QY 129 RVRELESEVNLKLSSELKNAKE-EINVLHGRLEKLNLMNNIENYVDSKVANLTFVNSL 187
DB 106 MTQSKTCWMLK-TDKNXYQYENILY--LQEVSSNOKKI-FLLKQKIANLEL-----156
QY 188 DGKSKCPSQEQIQSRPVQHLIYKQSDYVAIGKRSESYRVTPPKRSSEFWYCDMETM 247
DB 157 --CQOQ-PCRDVQ---IQEFTCKDCQEVANKCARLSGLYIKFLKAKQQLVYCEIFS 210
QY 248 GGGTVLQARLDGSTNTRTWQDYKAGFG---NLRRFNLGNDKIHLLTKSKEM--ILR 301
DB 211 GSAVTIQRBLDGSVNFHKNVQYREGFYLSNDKTEFWLGNKIHLLTQSTQTIPIVNR 270
QY 302 IDLEDFNGVELYALYDCQFYVANFLKYRLHVGNV-NGTAGDAL-----RPNKHV-NH 351
DB 271 LEEDKSNQKSTADYSTIFRLGSEKDNVRYFYAFIGDAGDAFDGDFGDDPSDKFYTS 330
QY 352 DLKFTTPKXNDRYPSGNGLYVSSQWDFDACLSANLNGKYH-----OKYRGVRN 403
DB 331 NGMGFTFDKDNKCF-DGNCABQDGGGWYNRCHAAHLNGKYQGGTYSADSGSPGYDN 389
QY 404 GIFWGTW 410
DB 390 GILWATW 396

RESULT 13
A:JC5980
fibrin-A precursor - mouse
C:Species: Mus musculus (house mouse)
C:Date: 06-May-1998 #sequence_revision 29-May-1998 #text_change 18-Feb-2000
C:Accession: JC5980
R:Fujimori, Y.; Harumiya, S.; Fukumoto, Y.; Miura, Y.; Yagasaki, K.; Tachikawa, H.; Fu
Biochem. Biophys. Res. Commun. 244, 796-800, 1998
A:Title: Molecular cloning and characterization of mouse fibrin-A.
A:Reference number: JC5980; MUID:98205881; PMID:9535745
A:Accession: JC5980
A:Molecule type: mRNA
A:Residues: 1-334 <FCJ>
A:Cross-references: DDBJ:AB007813; NID:G2957011; PIDN:BAA25126.1; PID:G2:026054; PID:G2
C:Comment: This protein consists of both collagen- and fibrinogen- like domains.
C:Superfamily: fibrinogen beta/gamma homology
F:1-21/Domain: signal sequence #status predicted <SIG>
F:50-64,68-106/Domain: collagen-like #status predicted <COL>
F:123-334/Domain: fibrinogen beta/gamma homology <FBG>

Query Match 19.0%; Score 452; DB 2; Length 334;
Best Local Similarity 34.4%; Pred. No. 6.5e-24;
Matches 114; Conservative 35; Mismatches 106; Indels 76; Gaps 12;
QY 107 GDPGRNGLLLP--STGAPGEVDNRVRE-ESEVNLKLSSELKNAKEINVLHGRLEKLN 164
DB 74 GSPKMG---PAGSKGEPGTWPGPVKGEKGTGAAPS---LQEKELG-----115
QY 165 MNMNIENYVDSKVANLTFVNSLDGKSKCPSQEQIQSRPVQHLIYKQSDYVAIGKRSS 224
DB 116 -----DTLCQKGP-----RSCKDLTRGIFLT 137
QY 225 ETVRV-TPQPKNSSEFWYCDMETGGGWTVLQARLDGSTNTRTWQDYKAGFNLRSEFW 283
DB 138 GWYTIHLPDQR--PLTVLCMDVDGGGKTVFQRRVDGSDIFFFDWDSYKSGFNLGTETW 295
QY 284 LGNDKIHLLTKSKEMILRILEDENGVVELYALYDQFYVANFLKYRLHVGNV-NGTAGDA 342

Dz 241 LLSNLNGQY--DYSGAPS--YWSYLPGDNDQ:P-----FAEMKJNR 280

Search completed: November 5, 2003, 16:48:13
Job time : 28.0749 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 5, 2003, 15:59:02 ; Search time 19.3392 Seconds
(without alignments)
1067.536 Million cell updates/sec

Title: US-09-902-563-2

Perfect score: 2378

Sequence: 1 XMIAWYWLSSAVLATYGL.....GYKSFKEAKFMIRPMHFP 439

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 5

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_41.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2378	100.0	439	1 FGL2 HUMAN	Q14314 homo sapien
2	1853.5	77.9	432	1 FGL2 MOUSE	P12804 mus musculus
3	525	22.1	496	1 AGP2 MOUSE	O35608 mus musculus
4	524.5	22.1	375	1 AGP2 BOVIN	O77832 bos taurus
5	523	22.0	436	1 AGP2 PIG	C9b0y7 sus scrofa
6	522	22.0	496	1 AGP2 HUMAN	O15123 homo sapien
7	511.5	21.5	463	1 FIBB CHICK	Q02020 gallus gall
8	506.5	21.3	312	1 FGL1 HUMAN	Q08930 homo sapien
9	486.5	20.5	498	1 AGP1 HUMAN	C15389 homo sapien
10	485.5	20.4	493	1 ANL2 MOUSE	Q9r245 mus musculus
11	484.5	20.4	453	1 FIBG HUMAN	P02679 homo sapien
12	483.5	20.3	498	1 AGP1 MOUSE	O08538 mus musculus
13	480.5	20.2	493	1 ANL2 HUMAN	O9uk49 homo sapien
14	479.5	20.2	477	1 FIBB PETMA	P02678 petromyzon
15	473	19.9	497	1 AGP1 RAT	O35460 rattus norv
16	471	19.8	468	1 FIBB BOVIN	P02676 bos taurus
17	470.5	19.8	509	1 AGP4 MOUSE	C9wh06 mus musculus
18	467	19.6	481	1 AGP1 BOVIN	O18920 bos taurus
19	462	19.4	444	1 FIBG BOVIN	P12799 bos taurus
20	461	19.4	491	1 FIBB HUMAN	P02675 homo sapien
21	456	19.2	438	1 FIBG XENLA	P17634 xenopus lae
22	454.5	19.1	479	1 FIBB RAT	P14480 rattus norv
23	452	19.0	334	1 FCN1 MOUSE	O70165 mus musculus
24	451	19.0	866	1 FIBB HUMAN	P02671 homo sapien
25	450	18.9	503	1 AGP4 HUMAN	O9y264 homo sapien
26	446	18.8	282	1 FIBB PARPA	P19477 parastichop
27	441	18.5	782	1 FIBB RAT	PC6399 rattus norv
28	438.5	18.4	335	1 FCN1 RAT	Q9wts8 rattus norv
29	428.5	18.0	432	1 FIBG PETMA	P04315 petromyzon
30	428	18.0	339	1 FCN2 RAT	P57756 rattus norv
31	427.5	18.0	741	1 FIBB CHICK	P14448 gallus gall
32	427	18.0	326	1 FCN1 HUMAN	O00632 homo sapien
33	421.5	17.7	306	1 FCN2 MOUSE	O70497 mus musculus

RESULT 1

FGL2_HUMAN
ID FGL2_HUMAN STANDARD; PRT; 439 AA.
AC Q14314;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Fibrinogen precursor (Fibrinogen-like protein 2) (p749).
GN FGL2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Small intestine;
RX MEDLINE=95369700; PubMed=7642106;
RA Ruegg C., Pytel R.;
RT "Sequence of a human transcript expressed in T-lymphocytes and
RT encoding a fibrinogen-like protein.";
RL Gene 160:257-262(1995).
RW [2]
RP SEQUENCE FROM N.A.
RA Yuvaraj S., Liu X., Marsden P., Levy G.;
RT "Cloning and characterization of Fgl2: the human counterpart to the
RT mouse gene Fgl2.";
RJ Submitted (NOV-1998) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A., AND VARIANT GLU-53.
RA Rieder M.J., Arnel T.Z., Carrington D.P., Chung M.-W., Lee K.L.,
RA Poe C.L., Ozuna M., Yi Q., Nickerson D.A.;
RJ Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A.
RC TISSUE=Blood;
RX MEDLINE=22389257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Sherman C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Wax S., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong J.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udell T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellanc N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek C.A., Guraratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Sklarsky R.W., Touchman J.W., Green E.D., Dickens M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M., Skalska U., Smalls D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Maria M.A.;
RT "Generation and initial analysis of more than 15,000 full-length
RT human and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).

ALIGNMENTS

34	420	17.7	313	1	FCN2_HUMAN	Q15485 homo sapien
35	419	17.6	445	1	FIBG_RAT	PC2680 rattus norv
36	414.5	17.4	299	1	FCN1_HUMAN	O75636 homo sapien
37	399	16.8	255	1	MFA4_HUMAN	P55083 homo sapien
38	397.5	16.7	4289	1	TENX_HUMAN	P22105 homo sapien
39	394.5	16.6	460	1	ANG3_HUMAN	O9y5c1 homo sapien
40	388	16.3	2201	1	TENA_HUMAN	P24821 homo sapien
41	386.5	16.3	1746	1	TENA_PIG	Q23116 sus scrofa
42	386	16.2	1808	1	TENA_CHICK	P10039 gallus gall
43	374.5	15.7	465	1	ANL4_HUMAN	C9b0y76 homo sapien
44	374.5	15.7	455	1	ANL3_MOUSE	O9y182 mus musculus
45	369	15.5	410	1	ANL4_MOUSE	O9z1p3 mus musculus

[5]
 CHARACTER:ZATT:CN.
 RX MEDLINE=98309432; PubMed=9647217;
 RA Marazzi S., Blum S., Hartmann R., Gundersen D., Schreyer M.,
 RA Argaves S., von Fliedner V., Pytela R., Ruegg C.;
 RT "Characterization of human fibrocytes, a fibrinogen-like protein
 secreted by T lymphocytes.";
 RL J. Immunol. 161:138-147(1998).
 CC -!- FUNCTION: MAY PLAY A ROLE IN PHYSIOLOGIC LYMPHOCYTE FUNCTIONS AT
 CC MUCOSAL SITES.
 CC -!- SUBUNIT: HOMOTETRAVER; DISULFIDE-LINKED.
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- TISSUE SPECIFICITY: CONSTITUTIVELY EXPRESSED IN CYTOTOXIC
 CC T-CELLS.
 CC -!- SIMILARITY: Contains 1 fibrinogen C-terminal domain.
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 CC
 CC EMBL: Z36531; CA885298; -;
 CC EMBL: AF104015; AAD1825.1; -;
 CC EMBL: AF104014; AAD1825.1; JOINED.
 CC EMBL: AF468959; AAL68855.1; -;
 CC EMBL: BC033820; AAH33820.1; -;
 CC EMBL: I37391; I37391;
 CC HSSP: P02671; 1F2D.
 CC Genew: HGNC:3696; FGL2.
 CC MIM: 603351; -;
 CC GO: GO:0005576; C:extracellular; TAS.
 CC GO: GO:0005973; C:fibrinogen beta chain; TAS.
 CC GO: GO:0005974; C:fibrinogen gamma chain; TAS.
 CC InterPro: IPR002181; Fibrinogen_C.
 CC Pfam: PF00147; fibrinogen_C; -;
 CC SMART: SM00186; FBG; 1.
 CC PROSITE: PS00534; FIBRIN_AG_C_DOMAIN; 1.
 CC T-cell: Glycoprotein; Signal; Polymorphism.
 CC SIGNAL: 23
 CC POTENTIAL.
 CC CHAIN 24 439
 CC FIBROLEUKIN.
 CC DOMAIN 210 435
 CC FIBRINOGEN C-TERMINAL.
 CC DISULFID 213 242
 CC BY SIMILARITY.
 CC DISULFID 371 384
 CC BY SIMILARITY.
 CC CARBOHYD 25 25
 CC N-LINKED (GLCNAC...); (POTENTIAL).
 CC CARBOHYD 179 179
 CC N-LINKED (GLCNAC...); (POTENTIAL).
 CC CARBOHYD 235 235
 CC N-LINKED (GLCNAC...); (POTENTIAL).
 CC CARBOHYD 263 263
 CC N-LINKED (GLCNAC...); (POTENTIAL).
 CC CARBOHYD 336 336
 CC N-LINKED (GLCNAC...); (POTENTIAL).
 CC VARIANT 53 53
 CC G -> E.
 CC /FTID=VAR_013066.
 CC
 CC SEQUENCE 439 AA; 50228 MW; DF34656288B49E68 CRC64;
 CC
 CC Query Match 100.0%; Score 2378; DB 1; Length 439;
 CC Best Local Similarity 100.0%; Pred. No. 2.4e-153;
 CC Matches 439; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 CC
 CC 1 MKLANWYLLSSAVLATYGFVAVANNETEEIKDERAKDVCPVR-LESRGKGEAGECPYQVS 60
 CC
 CC 1 MKLANWYLLSSAVLATYGFVAVANNETEEIKDERAKDVCPVR-LESRGKGEAGECPYQVS 60
 CC
 CC 61 LPPITIQLPKQFRIEVEFVKQLKEIVNSLKKSCQCKLQADNDGPGNGLLLPSTG 120
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 CC 121 APGEVGNRRVRESEFVKLSSELKNAKEEIVNLHGLEKLNLVANNIENYDCKVAIL 180
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 CC 181 TFVNSLDGKCKSPCEQIQSRPVQHLIYKCCSDYYAIGKRSETYRVTPDPKSSFEV 240
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Db 181 TFVNSLDGKCKSPCEQIQSRPVQHLIYKCCSDYYAIGKRSETYRVTPDPKSSFEV 240
 Qy 241 YCDMETWGGGKTVLQARLDGSTNFTRTWQDYKAGFGNLRREFWLGNDKIHLLTKSKEMIL 300
 Db 241 YCDMETWGGGKTVLQARLDGSTNFTRTWQDYKAGFGNLRREFWLGNDKIHLLTKSKEMIL 300
 Qy 301 RIDLEDNGVELYALYDQFYVANEFLKYRLHVGNYGTAGDALRFNKHYNHDLKFFFTPD 360
 Db 301 RIDLEDNGVELYALYDQFYVANEFLKYRLHVGNYGTAGDALRFNKHYNHDLKFFFTPD 360
 Qy 361 KNDRVPSGNGGLYYSSGWWFADCLSANLNGKYVHKYRGVNRNGIETWGTWPGYSEAHPGG 420
 Db 361 KNDRVPSGNGGLYYSSGWWFADCLSANLNGKYVHKYRGVNRNGIETWGTWPGYSEAHPGG 420
 Qy 421 YKGSFKKAKMMIRPKPKP 439
 Db 421 YKGSFKKAKMMIRPKPKP 439
 CC
 CC RESULT 2
 CC FGL2_MOUSE
 CC ID FGL2_MOUSE STANDARD; PRT; 432 AA.
 CC AC P12804;
 CC DT 01-OCT-1989 (Rel. 12, Created);
 CC DT 01-OCT-1989 (Rel. 12, Last sequence update);
 CC DT 16-OCT-2001 (Rel. 42, Last annotation update);
 CC DE Fibrinogen precursor (fibrinogen-like protein 2) (Prothrombinase)
 CC DE (Cytotoxic T-lymphocyte specific protein).
 CC GN FGL2 OR FIBLP.
 CC OS Mus musculus (Mouse).
 CC CC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 CC CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus; Mus.
 CC CC NCBI_TaxID:10090;
 CC RN 1.
 CC RP SEQUENCE FROM N.A.
 CC PC TISSUE=Cytotoxic T-cell;
 CC RX MEDLINE=87175527; PubMed=3550794;
 CC RA Koyana T., Hall J.R., Hasegawa M., Teraoka S., Saito H.;
 CC RT "Structure of a cytotoxic T-lymphocyte-specific gene shows a strong
 CC RT homology to fibrinogen beta and gamma chains.";
 CC R1 Proc. Natl. Acad. Sci. U.S.A. 84:1609-1613(1987).
 CC RN 2.
 CC RP SEQUENCE FROM N.A. AND CHARACTERIZATION.
 CC RC STRAIN=BALB/CJ; TISSUE=Peritoneal macrophage;
 CC RX MEDLINE=95333285; PubMed=7609073;
 CC RA Parr R.L., Fung L., Reneker J., Myers-Kasor N., Leibowitz J.L.,
 CC RA Levy G.;
 CC RT "Association of mouse fibrinogen-like protein with murine hepatitis
 CC RT virus-induced prothrombinase activity.";
 CC RL J. Virol. 69:5033-5038(1995).
 CC CC -!- FUNCTION: CONVERTS PROTHROMBIN TO THROMBIN.
 CC CC -!- SUBUNIT: HOMOTETRAMER; DISULFIDE-LINKED (BY SIMILARITY).
 CC CC -!- SUBCELLULAR LOCATION: Secreted.
 CC CC -!- TISSUE SPECIFICITY: CONSTITUTIVELY EXPRESSED IN CYTOTOXIC
 CC T-CELLS.
 CC CC -!- INDUCTION: IN MACROPHAGES, DURING INFECTION BY MOUSE HEPATITIS
 CC VIRUS STRAIN 3 (MHV-3).
 CC CC -!- SIMILARITY: Contains 1 fibrinogen C-terminal domain.
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 CC
 CC EMBL: M16238; AAA37624.1; -;
 CC EMBL: M15761; AAA37624.1; JOINED.
 CC EMBL: S78773; AAB34823.1; -;
 CC PIR: A27447; A27447.
 CC HSSP: P02671; 1F2D.
 CC MGD: MG1:103266; Fgl2.


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DR InterPro; IPR002181; Fibrinogen C.
DR Pfam; PF00147; fibrinogen_C; 1.
DR SMART; SM00186; FBG; 1.
DR PROSITE; PS00514; FIBRIN AG_C_DOMAIN; 1.
KW T-cell; Cytolysis; Signal.
FT SIGNAL 1 19
FT CHAIN 20 432
FT DOMAIN 203 428
FT DISULFID 206 235
FT DISULFID 364 377
FT CARBOHYD 24 24
FT CARBOHYD 172 172
FT CARBOHYD 228 228
FT CARBOHYD 256 256
FT CARBOHYD 329 329
FT CONFLICT 332 332
FT SEQUENCE 432 AA; 48951 MW; 2B297F69CCB4A782 CRC64;
Query Match 77.9%; Score 1853.5; DB 1; Length 432;
Best Local Similarity 77.7%; Pred. No. 5.8e-116;
Matches 341; Conservative 42; Mismatches 49; Indels 7; Gaps 4;
QY 1 MRLANWYLSAVLATYGLVANNETEEIKDERAKDVPVRLESRGKCEEAGECPYCVS 60
DB 1 MRLPCMLWLSAVLAACR-AVEEHNLTGLEDASAAACPARLEGSGRC-EGSQCPFLT 58
QY 61 LPPLTIQLPKQFSRIEVEFKVQNVKEIVNSLKKSCDCKLOADNGDPRNGLLPSTG 120
DB 59 LPPLTIQLPKQFSRIEVEFKVQNVKEIVNSLKKSCDCKLOADNGDPRNGLLPSTG 114
QY 121 AFGEVGNRVRELESEVKNLSSELKNVLEKLNLMNMIENYVDSKYAVL 160
DB 115 AE-TAEDSRVRELESEVKNLSSELKNVLEKLNLMNMIENYVDSKYAVL 173
QY 181 TFVNSLDGKSKCPQSQIQSRPVCHLIYKDCSDYYAIGKRSEETRYVTPDPKNSFEV 240
DB 174 TFVNSLDGKSKCPQSQIQSRPVCHLIYKDCSDYYAIGKRSEETRYVTPDPKNSFEV 233
QY 241 YCDXETMGGGTVALQARLDGSTNFTRWQDYKAGFNLRRSFWLGNKIHLLTSKEMIL 300
DB 234 YCDXETMGGGTVALQARLDGSTNFTRWQDYKAGFNLRRSFWLGNKIHLLTSKEMIL 293
QY 301 RIDLEDFNGVELYALDYQFYVANEFLKYRHLHGVNNGTAGDALRPNKYNHCLKFFTPD 360
DB 294 RIDLEDFNGVELYALDYQFYVANEFLKYRHLHGVNNGTAGDALRPNKYNHCLKFFTPD 353
QY 361 KDNRYPSGNGCLYSSGWMFJACLSANLNGKYHOKYKGVNRNGIFWCTWFCVSEAHPGG 420
DB 354 KDNRYPSGNGCLYSSGWMFJACLSANLNGKYHOKYKGVNRNGIFWCTWFCVSEAHPGG 413
QY 421 YKSSPFKEAKYKATSPQFKP 439
DB 414 YKSSPFKEAKYKATSPQFKP 432
RESULT 3
ACGP2_MOUSE
ID ACGP2_MOUSE STANDARD; PRT; 496 AA.
AC O356C8;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Angiopoietin-2 precursor (ANG-2).
GN ANGPT2 OR AGPT2.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN (1)
RP SEQUENCE FROM N.A.
RC TISSUE=Uterus;
RX MEDLINE=97349327; PubMed=9204896;
RA Maisonnier P.C., Suri C., Jones P.F., Bartunkova S., Wiegand S.C.,

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RA Radziejewski C., Compton D.L., McClain J., Aldrich T.H.,
RA Papadopoulos N., Daly T.C., Davis S., Sato T.N., Yancopoulos G.D.;
RT "Angiopoietin-2, a natural antagonist for Tie2 that disrupts in vivo
RT angiogenesis.";
RJ Science 277:55-60(1997).
CC -!- FUNCTION: BINDS TO TIE2 RECEPTOR AND COUNTERACTS BLOOD VESSEL
CC MATURATION/STABILITY MEDIATED BY ANGIOPOIETIN-1. ITS FUNCTION MAY
CC BE CONTEXT-DEPENDENT. IN THE ABSENCE OF ANGIOGENIC INDUCERS, SUCH
CC AS VEGF, ANG2-MEDIATED LOOSENING OF CELL-MATRIX CONTACTS MAY
CC INDUCE ENDOTHELIAL CELL APOPTOSIS WITH CONSEQUENT VASCULAR
CC REGRESSION. IN CONCERT WITH VEGF, IT MAY FACILITATE ENDOTHELIAL
CC CELL MIGRATION AND PROLIFERATION, THUS SERVING AS A PERMISSIVE
CC ANGIOGENIC SIGNAL.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: EXPRESSED ONLY AT SITES OF VASCULAR
CC REMODELING.
CC -!- SIMILARITY: Contains 1 fibrinogen C-terminal domain.
CC
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CC
CC EMBL; AF004326; AAB63189.1; .
CC HSP; PC2671; IFZD.
CC WGD; MGI:1202890; Agpt2.
CC InterPro; IPR002181; Fibrinogen_C.
CC Pfam; PF00147; fibrinogen_C; 1.
CC SMART; SM00186; FBG; 1.
CC PROSITE; PS00514; FIBRIN AG_C_DOMAIN; 1.
CC Angiogenesis; Glycoprotein; Coiled coil; Signal.
FT SIGNAL 1 18.
FT CHAIN 19 496
FT DOMAIN 159 256
FT DOMAIN 280 496
FT DISULFID 284 313
FT DISULFID 437 450
FT CARBOHYD 89 89
FT CARBOHYD 119 119
FT CARBOHYD 133 133
FT CARBOHYD 151 151
FT CARBOHYD 240 240
FT CARBOHYD 304 304
FT SEQUENCE 496 AA; 56616 MW; FA3021FE4E01C410 CRC64;
Query Match 22.1%; Score 525; DB 1; Length 496;
Best Local Similarity 32.9%; Pred. No. 3e-28;
Matches 127; Conservative 65; Mismatches 154; Indels 40; Gaps 9;
QY 61 LPPLTIQLPKQFSRIEVEFKVQNVKEIVNSLKKSCDCKLOADNGDPRNGLLPSTG 120
DB 142 LTDEAQLVNTTL-----ELQLQHS-STNKLEKLDQTSINKLQWKSFL----- 19;
QY 121 APGEVGNRVRELESEVKNLSSELKNVLEKLNLMNMIENYVDSKYAVL 172
DB 192 -----EQKLVDEGHSEQLQSKYKQDELQVLSKQSSVIDELEKLVATVWKN--SL 243
QY 173 VDSKANLTFVNSLDGKSKCPQSQIQSRPVCHLIYKDCSDYYAIGKRSEETRYVTPD 232
DB 244 LQKQHDLMETVNSLTMKSSPNSSKSSVAIRKEEQTTFRDCAEIFKSGT:TSGIYTLTFP 303
QY 233 PKNSPFVYCDMETMGGGWTVALQARLDGSTNFTRWQDYKAGFNLRRSFWLGNKIHLL 292
DB 304 NSTEIKAYCDMVGCGGWTVIQHRDGSVDQFTWKEKEGFGNPLGEVWLGNEFVSQJ 363
QY 293 TKSKEMLRIDLEDFNGVELYALDYQFYVANEFLKYRHLHGVNNGTAGDALRPNKYNH 352
DB 364 TGQHYVYK:QLKDWEGNEAHSYDFYLAGEESNYRIHLTGLTGTAAKISSISQPSGD- 422
QY 353 LKFTTTPDKNDNRYPSGNGCLYSSGWMFJACLSANLNGKYHOKYKGVNR-NGIFWGTWP 411

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Db 423 ---FSTKDSNDKXC-KCQSM-SGGWDFACGPNLNGYYPKQNTNKFNGIKRYYXK 478
QY 412 GVSEAHPGGKYSFKEAKMMIRPKHF 437
Db 479 G-----SGY--SJKATTMMIRPADF 496

RESULT 4
AGP2_BOVIN STANDARD; PRT; 375 AA.
AC G77802: C9TSK0;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Angiopoietin-2 (ANG-2) (Fragment).
GN ANGPT2 OR ANG2.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
CC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Ovary.
RX MEDLINE=99054348; PubMed=9840613;
RA Goede V., Schmidt T., Kimina S., Kozian D., Augustin H.G.;
RT "Analysis of blood vessel maturation processes during cyclic ovarian
angiogenesis.";
RJ Lab. Invest. 78:1385-1394 (1998).
RP [2]
RP SEQUENCE OF 219-355 FROM N.A.
RC TISSUE=Adrenal cortex;
RX MEDLINE=98451564; PubMed=9778732;
RA Mandriota S.J., Pepper M.S.;
RT "Regulation of angiopoietin-2 mRNA levels in bovine microvascular
endothelial cells by cytokines and hypoxia.";
RJ Circ. Res. 83:852-859 (1998).
CC -!- FUNCTION: BINDS TO TIE2 RECEPTOR AND COUNTERACTS BLOOD VESSEL
MATURATION/STABILITY MEDIATED BY ANGIOPOIETIN-1. ITS FUNCTION MAY
BE CONTEXT-DEPENDENT. IN THE ABSENCE OF ANGIOGENIC INDUCERS, SUCH
AS VEGF, ANG2-MEDIATED LOOSENING OF CELL-MATRIX CONTACTS MAY
INDUCE ENDOTHelial CELL APOPTOSIS WITH CONSEQUENT VASCULAR
REGRESSION. IN CONCERT WITH VEGF, IT MAY FACILITATE ENDOTHelial
CELL MIGRATION AND PROLIFERATION, THUS SERVING AS A PERMISSIVE
ANGIOGENIC SIGNAL.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- DEVELOPMENTAL STAGE: FOUND TO BE EXPRESSED THROUGHOUT THE OVARIAN
CYCLE, OVEREXPRESSED DURING LUTEOLYSIS. THIS COULD REFLECT THE
REGRESSION OF CAPILLARIES THAT HAD DEVELOPED PERICYTE CONTACT IN
THE MIDSTAGE CORPUS LUTEUM.
CC -!- SIMILARITY: Contains 1 fibrinogen C-terminal domain.

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DR EMBL; AF094699; AAC62490.1; -;
DR EMBL; AF032924; AAC78285.1; -;
DR HSP; P02671; IFZD.
DR InterPro; IPRO02181; Fibrinogen_C.
DR Pfam; PF00147; fibrinogen_C; 1.
DR SMART; SM00186; FBG; 1.
DR PROSITE; PS00514; FIBRIN_AG_C_DOMAIN; 1.
KW Angiogenesis; Glycoprotein; Coiled coil.
FT NON_TER 1 1
FT DOMAIN 10 139 COILED COIL (POTENTIAL).
FT DOMAIN 159 375 FIBRINOGEN C-TERMINAL.
FT DISULFID 163 192 BY SIMILARITY.

FT DISULFID 316 329 BY SIMILARITY.
FT CARBOHYD 13 13 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 31 31 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 120 120 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 183 183 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CONFLICT 272 272 S -> L (IN REF. 2).
SQ SEQUENCE 375 AA; 42761 MW; 6F086C4A5C80050A CRC64;

Query Match 22.1%; Score 524.5; DB 1; Length 375;
Best Local Similarity 34.2%; Pred. No. 2.3e-28;
Matches 136; Conservative 58; Mismatches 139; Indels 65; Gaps 14;

QY 61 LPPLTIQLPKQFSRIEVEFKVQNLKEIV--NSLKSKQD-----CKLQADNDGPGRG 113
DB 22 LTDVEAQLNQTRL-----ELQLLESLSLNKLEKQLDQTSISKLQ-----DKNS 69
QY 114 LLLPSTGAPGEVDNRVRELESEVKNLSSELKNKEINVLHGR-----LEK-LNLVN 165
DB 70 FL-----EKKVLDMEKHIIVQRSIKERQQLQVLVSKNSIIELEKQLVTAT 118
QY 166 MNNI-----ENVDSKVANLTFVNSLDGKSKQFSQEQIOSRPVQHLYIKDCSDYYAIG 220
DB 119 VNSVLQKQCHDLMETVNNLLTLMSTSNPSYSLAKDECI-----IPRCGEAPKSG 170
QY 221 KESSEYRVTPDPKNSFEVYCDMETGSGMTVLQARLDGSGTNTRTWQDYKAGFGNLR 280
DB 171 LTTSGVYTLTFPNSTEE-KAYCDMETGGGWTIVQRREGSGVDFORTWKYKVGFGNPSG 230
QY 281 EFWLGNDRKIHLLTKSKEMILRLIDLEDFNGVELYALYDOFYVANEFKVLHVGNYNGTAG 340
DB 231 EHWLGNFVSQVGTQKRVVLKIH-LRDWEGNEAYSLYDHFYLSNEELNRYIHLKGLGTAG 290
QY 341 DALRPNKYNHDLKFPTTDPKNDRYPSGNGCLGYSSGWNFDACLSANLNKYYHQYKRG 400
DB 291 KISSISQFGND-----FSTKDAADKIC-KCSQMLTGGWDFACGPNLNGYYPKQNT 345
QY 401 VR-NGIFAGTWGVSEAHPGGKYSFKEAKMMIRPKHF 437
DB 346 NKENGIKRYWKG-----SGY--SLKATTMMIRPADF 375

RESULT 5
AGP2_PIG STANDARD; PRT; 496 AA.
AC G9BBY7;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Angiopoietin-2 precursor (ANG-2).
GN ANGPT2.
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9823;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21153163; PubMed=11230987;
RA Kim I., Moon S.O., Han C.Y., Pak Y.K., Moon S.K., Kim J.J., Koh G.Y.;
RT "The angiopoietin-tie2 system in coronary artery endothelium prevents
oxidized low-density lipoprotein-induced apoptosis.";
RJ Cardiovasc. Res. 49:872-881 (2001).
CC -!- FUNCTION: BINDS TO TIE2 RECEPTOR AND COUNTERACTS BLOOD VESSEL
MATURATION/STABILITY MEDIATED BY ANGIOPOIETIN-1. ITS FUNCTION MAY
BE CONTEXT-DEPENDENT. IN THE ABSENCE OF ANGIOGENIC INDUCERS, SUCH
AS VEGF, ANG2-MEDIATED LOOSENING OF CELL-MATRIX CONTACTS MAY
INDUCE ENDOTHelial CELL APOPTOSIS WITH CONSEQUENT VASCULAR
REGRESSION. IN CONCERT WITH VEGF, IT MAY FACILITATE ENDOTHelial
CELL MIGRATION AND PROLIFERATION, THUS SERVING AS A PERMISSIVE
ANGIOGENIC SIGNAL (by similarity).
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: Contains 1 fibrinogen C-terminal domain.

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CC -----
DR EMBL: AF233228; AAK4993.1; -.
DR HSSP: P02677; 1FZD.
DR InterPro: IPR002181; Fibrinogen_C.
DR Pfam: PF00147; fibrinogen_C_1.
DR SMART: SM00186; FBG_1.
DR PROSITE: PS00514; FIBRIN AG_C DOMAIN; 1.
KW Angiogenesis; Glycoprotein; Coiled coil; Signal.
FT SIGNAL 1 18
FT CHAIN 19 496
FT DOMAIN 130 255
FT DISULFID 284 313
FT DISULFID 437 450
FT CARBOHYD 89 89
FT CARBOHYD 119 119
FT CARBOHYD 133 133
FT CARBOHYD 151 151
FT CARBOHYD 240 240
FT CARBOHYD 304 304
SQ SEQUENCE 496 AA; 56911 MW; 33802BE224FE6B9D CRC64;
Query Match 22.0%; Score 523; DB 1; Length 496;
Best Local Similarity 34.9%; Pred. No. 4, 1e-28;
Matches 121; Conservative 49; Mismatches 120; Indels 57; Gaps 8;
QY 127 DNRVRELSSEVVKLS-----ELKVAKEINVLHRLKJMLVKN 168
Db 171 EKQILDQTSSEINKLQDKNSFLEKVKLDMEDKHIVCSIKKEKQGLQVSKQNSIIIEEL 230
QY 169 IENVYDSKAN-----TFVNSLDGCKKCPQCEQIQSRPVCHLIYK 211
Db 231 EKQLTATVNSVLQKQHDLMETVHNLMTISTNSAKHSLVAKEQI-----IFR 282
QY 212 DCSDYAIAIKRSSEYRYVTPDKNSSEFVYCDMETMGGGWITVQLARLQSGTNFRTWQDY 271
Db 283 DCAEAFKSLTSGTYTLTFPNSSTETKAYCDMETGGGWITVQPRDGSVDFORTAKY 342
QY 272 KAGFNLRREFWLNKDKHLTLTKSEMIJRDLDFNGVEYALYDQYVANEFKYRLH 331
Db 343 KMGFGSPSGEHLGNFEFVSQVTKRYLKIHLRDWEGNEAYSLYEHFYCSSEFNYRIH 402
QY 332 VQNYKSTAGDALRFRKXHNHDLKFTTPKCNDRYPGNGCYGYSXGWWFACLSANLNG 391
Db 403 LKGLTGTAGKISSISQPGND-----FSTKADNDKIC-KCSQMLTGGWFWFACGPSNLNG 457
QY 332 KYHOKYQGVGR-NGIFWGTGPGVSEAHPGGYSKSPKAEKMMIRPKHF 437
Db 458 MYVQRQNTKXFGIKRYWYKKG-----SGY--SLXA-TMMIRPADP 495
RESULT 6
AGP2 HUMAN STANDARD; PRT; 496 AA.
AC O1523; Q9NRR7; G9P2Y7;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Angiopoietin-2 precursor (ANG-2).
GN ANGPT2.
CS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORM 1).
RC TISSUE=Lung;

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RX MEDLINE-97349327; PubMed-9204896;
RA Maisorpierre P.C., Suri C., Jones P.F., Bartunkova S., Wiegand S.J.,
RA Radziejewski C., Compton D., McClain J., Aldrich T.H.,
RA Papadopoulos N., Daly T.J., Davis S., Sato T.N., Yancopoulos G.D.;
RT "Angiopoietin-2, a natural antagonist for Tie2 that disrupts in vivo
RT angiogenesis.",
AL Science 277:55-60(1997).
RK [2]
RP SEQUENCE FROM N.A. (ISOFORM 1).
RX MEDLINE-99126459; PubMed-9927494;
RA Takaka S., Mori M., Sakamoto Y., Makuchi M., Sugimachi K.,
RA Wards J.P.;
RT "Biologic significance of angiopoietin-2 expression in human
RT hepatocellular carcinoma.",
RL J. Clin. Invest. 103:341-345(1999).
RN [3]
RP SEQUENCE FROM N.A. (ISOFORM 2).
RC TISSUE=Umbilical vein endothelial cells;
RX MEDLINE-20309815; PubMed-10766762;
RA Kim S., Kim J.-H., Ryu Y.S., Jung S.H., Nah J.J., Koh G.Y.;
RT "Characterization and expression of a novel alternatively spliced
RT human angiopoietin-2.",
RL J. Biol. Chem. 275:18550-18556(2000).
CC -1- FUNCTION. BINDS TO TIE2 RECEPTOR AND COUNTERACTS BLOOD VESSEL
CC MATURATION/STABILITY MEDIATED BY ANGIOPOETIN-1. ITS FUNCTION MAY
CC BE CONTEXT-DEPENDENT. IN THE ABSENCE OF ANGIOPOETIN-1, ITS FUNCTION MAY
CC AS VEGF, ANG2-MEDIATED LOOSENING OF CELL-MATRIX CONTACTS MAY
CC INDUCE ENDOTHELIAL CELL APOPTOSIS WITH CONSEQUENT VASCULAR
CC REGRESSION. IN CONCERT WITH VEGF, IT MAY FACILITATE ENDOTHELIAL
CC CELL MIGRATION AND PROLIFERATION, THUS SERVING AS A PERMISSIVE
CC ANGIOGENIC SIGNAL.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=2;
CC Name=1;
CC IsoId=O15123.1; Sequence-Displayed;
CC Name=2;
CC IsoId=O15123.2; Sequence=VSP_001540;
CC -1- SIMILARITY: Contains 1 fibrinogen C-terminal domain.
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: AF004327; AAB63190.1; -.
DR EMBL: AB009865; BAA95590.1; -.
DR EMBL: AF187858; BAF78526.1; -.
DR HSSP: P02677; 1FZD.
DR Genew: HGNC:485; ANGPT2.
DR MIM: 601922; -.
DR GO: GO:0005615; C:extracellular space; TAS.
DR GO: GO:0005102; F:receptor binding activity; TAS.
DR GO: GO:003851; P:cell growth and/or maintenance; TAS.
DR GO: GO:0007165; P:signal transduction; TAS.
DR InterPro: IPR002181; Fibrinogen_C.
DR Pfam: PF00147; fibrinogen_C_1.
DR SMART: SM00186; FBG_1.
DR PROSITE: PS00514; FIBRIN AG_C DOMAIN; 1.
KW Angiogenesis; Glycoprotein; Coiled coil; Signal; Alternative splicing.
FT SIGNAL 1 16
FT CHAIN 17 496
FT DOMAIN 130 256
FT DOMAIN 280 496
FT DISULFID 284 313
FT DISULFID 437 450
FT CARBOHYD 89 89
FT CARBOHYD 119 119
FT CARBOHYD 133 133
FT CARBOHYD 151 151

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FT CARBOHYD 240 240 N-LINKED (GLNAC...) (POTENTIAL)
FT CARBOHYD 304 304 N-LINKED (GLNAC...) (POTENTIAL)
FT VARSPLIC 97 148 Missing (in isoform 2)
FT 268 268 MISSING (IN REF. 2)
FT CONFLICT 268 268 MISSING (IN REF. 2)
SQ SEQUENCE 496 AA; 56913 XA; 5642A58847A7385C CRC64;

Query Match 22.0%; Score 522; DB 1; Length 496;
Best Local Similarity 27.9%; Pred. No. 4; Se-28;
Matches 138; Conservative 74; Mismatches 159; Indels 124; Gaps 15;

QY 43 LESSRGKE---EAGECPYQVSLPPL-----TIQ--LPKQPSRIEEVFKEVQN 84
DB 26 MDSIGKQVQVQHGSCSYTFJPEWNCRCSSSPYVNAVQDALEVDSDVQRIQVLEN 85
QY 85 LKE-----IVNLSKSCQCKLQADNDGPGRNGLLSTGAPGVEGDN----- 128
DB 86 IMENNTQWLKLENYIQDNKXEMVEIQNAVQV-----QTAVWIEGTNLLNQ 134
QY 129 -----RVRELESEV-----NKLSSLEKVAKEEINVJHGR-----LEKL 161
DB 135 TABQTRKLTDEVAQVLNQTTRELUOLLEHSLSTNKLEKQILDCTSEENKLDQKNSFLEKK 194
QY 162 NLV-----NMNN-ENVYVDSKVANLTP-----V 183
DB 195 VLAMEDKHIIQLCSIKEEKDQLOLVYSKONSIEELEKAIIVATVNSVJQKQCHLNET 254
QY 194 VNSLDQKCKPSCQEQIQSRPVQHLIYKQCSYDYYAIGKSSSTYVTPDPKNSSEVYCD 243
DB 255 VNNLLTMTSNTSNAKOPTVAKEEQISIFROCAEVFKSGHTTNGIYTTFPNSTEETKAYCD 314
QY 244 METMGSGTWTVLQARLDGNTFTRTWCYKAGFNGLRREFNLGNDKIHILTKSKEMILRID 303
DB 315 MEAGGGWTIIQRRESGVDFRTWKYKVGFGNPSGEYVWLNFEVQSQTNQRTVJLKH 374
QY 304 LEDFNGVELYALDQPYVANEFLKYRHYGVNYNGTAGDALRFRKGYNHDLKFTTPOCKN 363
DB 375 LKDWEGNEAYSLYEHFYLSSSELYRIHJLKGLTGTAGKSSISQPGND---FSKQGEN 430
QY 364 DRYPSNGCUGYSSSGWFWFACLSANLNGYKQKYGVR-NGIFGTWPGVSEAHFGYK 422
DB 431 DKICIC-KCSQVLTGGMWFDACGPNLNGMYVFORQNTKFNGLKYYWAG-----SGY- 482
QY 423 SSFKEAKMIRPKHF 437
DB 483 -SUKATTMMIRPADF 496

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RESULT 7

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FIBB_CHICK STANDARD; PRT; 463 AA.
AC QG2020;
DT 01-JUL-1993 (Rel. 26, Created;
DT 01-JUL-1993 (Rel. 26, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Fibrinogen beta chain precursor [Contains: Fibrinopeptide B]
DE (Fragment).
GN FCB.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A., AND SEQUENCE OF 1-13 AND 18-39.
RX MEDLINE=91182745; PubMed=2009266;
RA Weissbach L., Oddoux C., Procyk R., Grieninger G.;
RT "The beta chain of chicken fibrinogen contains an atypical thrombin
RT cleavage site.";
RL Biochemistry 30:3230-3294(1991).
CC -!- FUNCTION: FIBRINOGEN HAS A DOUBLE FUNCTION: YIELDING MONOMERS THAT
CC POLYMERIZE INTO FIBRIN AND ACTING AS A COFACTOR IN PLATELET
CC AGGREGATION.

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-!- SUBUNIT: HEXAMER CONTAINING 2 SETS OF 3 NONIDENTICAL CHAINS
-!- (ALPHA, BETA AND GAMMA), LINKED TO EACH OTHER BY DISULFIDE BONDS.
-!- MISCELLANEOUS: CONVERSION OF FIBRINOGEN TO FIBRIN IS TRIGGERED BY
-!- THROMBIN, WHICH CLEAVES FIBRINOPEPTIDES A AND B FROM ALPHA & BETA
-!- CHAINS, AND THUS EXPOSES THE N-TERMINAL POLYMERIZATION SITES
-!- RESPONSIBLE FOR THE FORMATION OF THE SOFT CLOT. THE SOFT CLOT IS
-!- CONVERTED INTO THE HARD CLOT BY FACTOR XIII WHICH CATALYZES THE
-!- ESTERON-(GAMMA-GLUTAMYL)LYSINE CROSS-LINKING BETWEEN GAMMA CHAINS
-!- (STRONGER) AND BETWEEN ALPHA CHAINS (WEAKER) OF DIFFERENT
-!- MONOMERS.
-!- SIMILARITY: Contains 1 fibrinogen C-terminal domain.

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or send an email to license@isb-sib.ch).

EMBL; M58514; AAA48770.1; -.
PDB; A38463; A38463.
PDB; 1EI3; 10-MAY-00.
InterPro; IPR002181; Fibrinogen_C.
Pfam; PF00147; fibrinogen_C; 1.
SMART; SM00186; FBG; 1.
PROSITE; PS00514; FIBRIN_AG_C_DOMAIN; 1.
KW Blood coagulation; Plasma; Platelet; Glycoprotein; Sulfation;
KW 3D-structure.
FT MCV TER 1
FT PEPTIDE < 17 FIBRINOPEPTIDE B.
FT CHAIN 18 463 FIBRINOGEN BETA CHAIN.
FT MOD RES 5 5 SULFATION (BY SIMILARITY)
FT SITE 17 18 CLEAVAGE (BY THROMBIN; RELEASE
FT DISULFID 69 69 FIBRINOPEPTIDE B).
FT DISULFID 80 80 INTERCHAIN (WITH ALPHA) (BY SIMILARITY)
FT DISULFID 84 84 INTERCHAIN (WITH ALPHA) (BY SIMILARITY)
FT DISULFID 197 197 INTERCHAIN (WITH GAMMA) (BY SIMILARITY)
FT DISULFID 201 201 INTERCHAIN (WITH ALPHA) (BY SIMILARITY)
FT DISULFID 205 289 BY SIMILARITY.
FT DISULFID 215 244 BY SIMILARITY.
FT CASOHVD 367 410 BY SIMILARITY.
FT SEQUENCE 463 AA; 52678 MW; 204CD49BA79EC7B CRC64;

Query Match 21.5%; Score 511.5; DB 1; Length 463;
Best Local Similarity 30.4%; Pred. No. 2; Se-27;
Matches 137; Conservative 71; Mismatches 154; Indels 89; Gaps 16;

QY 31 KDERAKDVCVRLESQKQ-----EEAGE-CPYQVSLPPLTIQLPKQPSR;EEVFKEVQN- 84
DB 51 QDQKQMKKGIITPDAGGCKHPLDELGVJCTQCE---LQTLKQEKTKVQPVRLKDR 107
QY 85 -----LKEIVSLKSKSCQCKLQADNDGPGRNGLLSTGAPGVEGDNVRELE 134
DB 108 VAKFSDTSTWYQVNMIDNKLKVTQKQKD-----NDIILSEYNTENELHNYIK--D 159
QY 135 SEVVKLSSELAKNAKEEINVJHGRLEKLVNMNNIENVYDSKVANLTFVNSLDGKSKC 194
DB 160 NLQNNIPSSLRVLAVIDSLHKKIQKL-----ENAIATQT-----DYCRSPC 201
QY 195 PSQEQIOSRPVCHLIYKQCSYDYYAIGKRSSETYRVTDPKNSSEFVYCDMETGGGWTVL 254
DB 202 -----VASCNIPVVSGRECEDIYRKGETSEMIIQDPPTTPYRYCDMETDNGWTLI 256
QY 255 QARLDGSGTNTFTWQDYKAGFGNLLR-----EFWLGNDKTHLTKSKEMILRID 303
DB 257 QNRQDGSVNFGRADWEYKRGFGNIAKSGGKKYCDTPEGYWLGNDKLSQLTKIGTKVLE 316
QY 304 LEDFNGVELYALDQPYVANEFLKYRHYGVNYNGTAGDALR--FNHYN-----HDLK 354
DB 317 MEDWNGDKVSALYGGFTIHNEGNKYQLSVSNYKGNAGNALMEGASQLYGENRTYTT-HNGM 376

```

Cy 355 FFTTPDKNDRY----PSGNCGLYSSWFDACLSANLNGKY-----HOKYRGVFN 403
 Db 377 YFSTYDRNDGLATDPRKQCKSKGGGWNRYNCHAAENGRYWGTYSDWYAI:3:DD 436
 Qy 404 GIFTGTPGVSEAHFGGKVSFKKAKYMRP 434
 Db 437 GIVNRWKG-----SWY-SKKQMSMKIKP 450

RESULT 8
 FGL1_HUMAN
 ID FGL1_HUMAN STANDARD; ERT: 312 AA.
 AC Q08830; Q36K06; G96Q06;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Fibrinogen-like protein 1 precursor (Hepatocyte-derived fibrinogen-related protein 1) (HFRP-1) (Hepassocin) (HP-541).
 GN FGL1 OR HFRP1.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 CX NCBI_TaxID=9606;
 RN 1.
 RP SEQUENCE FROM N.A.
 RX TISSUE=Liver;
 RA YAMAMOTO T., GOTOH M., SASAKI H., TERADA M., KITAJIMA M., HIRAHASHI S.,
 RT "Molecular cloning and initial characterization of a novel fibrinogen-related gene, HFRP-1.";
 RL Biochem. Biophys. Res. Commun. 193:681-697(1993).
 RN [2]
 RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
 RX TISSUE=Liver;
 RA HARA H., YOSHIMURA H., UCHIDA S., TOYODA Y., AOKI M., SAKAI Y., MORIMOTO S., SHIOKAWA K.,
 RT "Molecular cloning and functional expression analysis of a cDNA for human heparosin, a liver-specific protein with hepatocyte mitogenic activity.";
 RL Biochim. Biophys. Acta 1520:45-53(2001).
 RN [3]
 RP SEQUENCE FROM N.A.
 RX TISSUE=Liver;
 RA STRAUSBERG R.L., FEINGOLD E.A., GROUSE L.H., DERGE J.G., KLAUSNER R.C., COLLINS F.S., WAGNER L., SHENMEN C.M., SCHULER G.D., ALTSCHUL S.F., ZEEBERG B., BUETOW K.H., SCHAEFER C.F., BHAT N.K., HOPKINS R.F., JORDAN H., MOORE T., MAX S.I., WANG J., HSIEH F., DIACHENKO L., MARUSINA K., FARMER A.A., RUBIN G.M., HONG L., STAPLETON M., SOARES M.B., BONALDO M.F., CASAVANT C.L., SCHEETZ T.E., BROWNSTEIN M.J., USLIN T.B., TOSHIYUKI S., CARINCI P., PRATGE C., RAHA S.S., LOQUELLANO N.A., PETERS G.C., ABRAMSON R.D., MULLAHS S., BOSAK S.A., MCEWAN P.J., MCKERNAN K.J., MAJEK J.A., GUNAKATTE P.H., RICHARDS S., WRIELEY K.C., HALE S., GARCIA A.M., GAY L.J., HULYK S.W., VILLALON D.K., MURZY D.M., SODERGREN E.J., LU X., GIBBS R.A., FAHEY J., HELTON E., KETTEMAN X., MADAN A., RODRIGUES S., SANCHEZ A., WHITING M., MADAN A., YOUNG A.C., SHEVCHENKO Y., BOUFFARD G.G., BLAKESLEY R.W., TOUCHMAN J.W., GREEN E.D., DICKSON M.C., RODRIGUEZ A.C., GRIMWOOD J., SCHUTZ J., MYERS R.M., BUTTERFIELD Y.S.N., KRZYWINSKI M.J., SKALSKA U., SMALUS D.E., SCHNERCH A., SCHEIN C.E., JONES S.C.M., MARRA M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 CC 1- FUNCTION: Has hepatocyte mitogenic activity.
 CC 1- SUBUNIT: Homodimer (Probable).
 CC 1- SUBCELLULAR LOCATION: Secreted.
 CC 1- TISSUE SPECIFICITY: Liver-specific.
 CC 1- SIMILARITY: Contains 1 fibrinogen C-terminal domain.

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 CC
 DR EMBL; D14446; BAA03336.1; -;
 DR EMBL; D87342; BAB70690.1; -;
 DR EMBL; BC007047; AAH07047.1; -;
 DR PIR; C05596; JN0596.
 DR HSSP; P22671; IFZD.
 DR Genew; HSNCL3695; FGL1.
 DR XIM; 605776; -;
 DR GO; GO:0005577; C:fibrinogen complex; TAS.
 DR InterPro; IPR002181; Fibrinogen_C.
 DR Pfam; PF00147; fibrinogen_C; 1.
 DR SMART; SM00186; FBG; 1.
 DR PROSITE; PS00514; FIBRIN_AG_C_DOMAIN; 1.
 KW Signal.
 FT CHAIN 1 22 FIBRINOGEN-LIKE PROTEIN 1.
 FT DOMAIN 23 312 FIBRINOGEN C-TERMINAL.
 FT DISULFID 26 26 INTERCHAIN (POTENTIAL).
 FT DISULFID 83 112 BY SIMILARITY.
 FT DISULFID 248 261 BY SIMILARITY.
 FT CONFLICT 15 15 I -> T (IN REF. 3).
 FT CONFLICT 69 69 N -> D (IN REF. 1).
 FT CONFLICT 72 72 I -> V (IN REF. 1).
 FT CONFLICT 105 105 P -> L (IN REF. 2).
 SQ SEQUENCE 312 AA; 36391 MW; 26BC82124E6660C2 CRC64;
 Query Match 21.3%; Score 506.5; DB 1; Length 312;
 Best Local Similarity 36.8%; Pred. No. 2.9e-27;
 Matches 119; Conservative 40; Mismatches 119; Indels 45; Gaps 10;
 Qy 131 RELESEVKNLSSELKNAKEEINVLHGRL-----KLNLVNANNIENVDSKANLTFVNS 186
 Db 18 REI-SAEEDCAQEMRLRAQVRULETRVQQQVKIKQLQENEVQFLDKGDENTVIDLG- 75
 Qy 187 LDKCKSCPSQEQIQSRFVQHLKYKCSYYAIGKRSSTYRTVPDPKNSFFVYCDMET 246
 Db 76 -----SKRQ-----YADCSFINDGKLSGFKIKPLQSPAFSVYCDMSD 116
 Qy 247 MGGWTVLQARLDGSTNFTTWQDYKAGPNL---RREFWGNDKIHLTKSKEXILRID 303
 Db 117 -GGGWTVIQRSDGSENFNRGWDYENGFGNFGVQHGFWLGNKLNHLFTTQEDYTLKID 175
 Qy 304 LEDFNGVELYALYDQFYVANEFLKYLHGVNNGTAGDALRFNKH-----YHCLKFFT 357
 Db 176 LADEKNSRYAQYKNFKVGDEKRFYELNIGEYSGTAGDSLGNFHPFVQWASHQRMKFS 235
 Qy 358 TPKNDNDRYPSGNGGLYSSGWMFADCLSANLNGKYHOKYRG-VRNGIFWGTWPGVSEA 416
 Db 236 TWDRHDNY-EGNCAEEDQSGWFWNCRNSANLNGVYSGPYTAKTNGIVKWTM----- 288
 Qy 417 HPGGYKSSFKKAKYMRPQKFKP 439
 Db 289 --HGWWYSLKSVVMKIRPNDFIP 309

RESULT 9
 AGP1_HUMAN
 ID AGP1_HUMAN STANDARD; PRT: 498 AA.
 AC Q15385;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Angiopoietin-1 precursor (ANG-1).
 GN ANGPT1 OR KIAA0003.
 OS Homo sapiens (Human).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

CC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A., AND VARIANT GLY-269 DEL.
RC TISSUE=Petal lung;
RX MEDLINE=97134663; PubMed=8980223;
RA Davis S., Aldrich T.H., Jones P.F., Acheson A., Compton D.L., Jain V.,
RA Ryan T.E., Bruno J., Radziejewski C., Maisonneuve P.C.,
RA Vancopoulos G.D.;
RT "Isolation of angiotensin-1, a ligand for the TIE2 receptor, by
RT secretion-trap expression cloning";
RL Cell 87:1161-1169(1996).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=22158633; PubMed=12168954;
RA Nakajima D., Okazaki N., Yarakawa H., Kikuno R., Ohara O., Nagase T.;
RA "Construction of expression-ready cDNA clones for KIAA genes: manual
RT curation of 330 KIAA cDNA clones";
RL DNA Res. 9:99-106(2002).
RN [3]
RP SEQUENCE OF 307-498 FROM N.A.
RC TISSUE=Bone marrow;
RX MEDLINE=96051387; PubMed=7594026;
RA Nomura N., Miyajima N., Suzuki T., Tanaka A., Kawarabayashi Y.,
RA Sato S., Nagase T., Seki N., Ishikawa K.-I., Tabata S.;
RT "Prediction of the coding sequences of unidentified human genes. I.
RT The coding sequences of 40 new genes (KIAA0001-KIAA0040) deduced by
RT analysis of randomly sampled cDNA clones from human immature myeloid
RT cell line KG-1";
RL DNA Res. 1:27-35(1994).
RN [4]
RP SEQUENCE FROM N.A., AND VARIANT GLY-269 DEL.
RA Shan Z.X., Yu X.Y., Lin Q.Y., Fu Y.H., Tan H.H., Zheng M., Lin S.G.;
RT "Human angiotensin-1 mRNA variant forms";
RL Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: BINDS AND ACTIVATES TIE2 RECEPTOR BY INDUCING ITS
CC TYROSINE PHOSPHORYLATION. IMPLICATED IN ENDOTHELIAL DEVELOPMENTAL
CC PROCESSES LATER AND DISTINCT FROM THAT OF VEGF. APPEARS TO PLAY A
CC CRUCIAL ROLE IN MEDIATING RECIPROCAL INTERACTIONS BETWEEN THE
CC ENDOTHELIUM AND SURROUNDING MATRIX AND MESENCHYME. MEDIATES BLOOD
CC VESSEL MATURATION/STABILITY. IT MAY PLAY AN IMPORTANT ROLE IN THE
CC HEART EARLY DEVELOPMENT.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- PTM: GLYCOSYLATED.
CC -!- MISCELLANEOUS: IT MAY HAVE A POTENTIAL THERAPEUTIC UTILITY SINCE
CC IT CAN BE USED FOR SPECIFICALLY TARGETING TUMOR VASCULATURE OR FOR
CC PROMOTING ANGIOGENIC PROCESSES IN CERTAIN ORGANS SUCH AS AN
CC ISCHEMIC HEART.
CC -!- SIMILARITY: Contains 1 fibrinogen C-terminal domain.
CC
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC use by non-profit institutions as long as its content is in no way
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CC
DR EMBL; U83508; AAB50557.1; -;
DR EMBL; D13628; BAA02793.2; ALT_INIT.
DR EMBL; AB084454; BAB91325.1; -;
DR EMBL; AV21564; AAM81745.1; -;
DR EMBL; AY224390; AAM92271.1; -;
DR HSSP; P02671; 1FZD.
DR Genbank; HGNC:484; ANGPT1.
DR MIM; 601667; -;
DR GO; GO:0005102; Fibrinogen binding activity; TAS.
DR GO; GO:0007165; P-signal transduction; TAS.

DR InterPro: IPR002181; Fibrinogen_C.
DR Pfam: PF0147; fibrinogen_C; 1.
DR SMART: SMCC186; FBG; 1.
DR PROSITE: PS00514; FIBRIN AG C-DOMAIN; 1.
KW Angiogenesis; Glycoprotein; Coiled coil; Signal; Polymorphism.
FT SIGNAL 1 15 POTENTIAL.
FT CHAIN 16 498 ANGIOPOIETIN-1.
FT DOMAIN 81 119 COILED COIL (POTENTIAL).
FT DOMAIN 153 261 COILED COIL (POTENTIAL).
FT DOMAIN 284 498 FIBRINOGEN C-TERMINAL.
FT DISULFID 286 315 BY SIMILARITY.
FT DISULFID 439 452 BY SIMILARITY.
FT CARBOHYD 92 92 N-LINKED (GLCNAC...) (POTENTIAL).
FT CARBOHYD 122 122 N-LINKED (GLCNAC...) (POTENTIAL).
FT CARBOHYD 154 154 N-LINKED (GLCNAC...) (POTENTIAL).
FT CARBOHYD 243 243 N-LINKED (GLCNAC...) (POTENTIAL).
FT CARBOHYD 295 295 N-LINKED (GLCNAC...) (POTENTIAL).
FT VARIANT 269 269 MISSING (IN CELL LINE T98G; MAY BE DUE TO
FT EXON SLIPPAGE).
FT /FTID=VAR_009940.
SQ SEQUENCE 498 AA; 57513 MW; 5D5FA63AEF6BE920 CRC64;
Query Match 20.5%; Score 486.5; DB 1; Length 498;
Best Local Similarity 32.3%; Pred. No. 1.2e-25;
Matches 131; Conservative 59; Mismatches 136; Indels 79; Gaps 16;
QY 61 LPLTIQLPQFGRIE-----EVKVEQNVNKEIVNSLKSCQCKLOADNDGDPGRN 112
DB 145 LTVDETQVNLQTSRLLEIQLIENSLSITYKLEKQLLQQTNEILKHE-----KN 192
QY 113 GLLLPSTGAPGVGNEVRELESEVKNLSSELKNAKEINVILHG-----RLEK-L 161
DB 192 SLL-----EKKILDEME---GKHELDTLKEEKENLQGLVTRQTYIQLLEKQL 237
QY 162 NLVNMNIENVDSKVANLTFVNSLDGKCK-----CPSCQEQIQSRFVQHLVYKCCSDYY 217
DB 238 NRTANN--SVLQKQQLLEMDTVHNLVNLCTKGVLKGGKREEKP-----FRDCADY 290
QY 218 AIGKRSETRV---TPDPNSSEFVYCDYMTGGGTVQARLDGSTFTFTWQDYKA 273
DB 291 QAGFNKSGIVTIVNNMPEK---KVFNCYDNGGGTIVQHRDGLSLEFQGWKEYKM 346
QY 274 GFGNLRREFGLRDKIHLTKSKXETILRIDLPNGVELVLYDQFYVANEFLKYLHLVG 333
DB 347 GFGNPSGEYMLGNEFFAITTSQYMLRIELMDWEGNRAYSQYDRFHIGNEKONYRUYCK 406
QY 334 NYNSTAGDALRFNKHYNHDLKFFTPDKNDNDYPSGNCGYYSGGWDFDACL SANLNGKY 393
DB 407 GHTGTAGKQSSLIHL-GAD---FSTKDADNDNCVC-KCALMLTGGWDFDAGGPNJNGMF 461
QY 394 YHC-KYRGVNGIFWGTWPGVSEAHPGGYKSSPKKAKMMIRPKHF 437
DB 462 YTAQNHGKLGNGIKWHYFKGPS-----YSLRSTTMMIRPLDF 498

RESULT 10

ANK2_MOUSE
ID ANK2_MOUSE STANDARD; PRT; 493 AA.
AC Q9R045;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Angiopoietin-related protein 2 precursor (Angiopoietin-like 2).
GN ANGPTL2 OR ARP2.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
CX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Heart;
RX MEDLINE=99403103; PubMed=10473614;
RA Kim I., Moor S.-O., Koh K.N., Kim H., Uhm C.-S., Kwak H.J., Kim N.-G.,

Koh G.Y.;

"Molecular cloning, expression, and characterization of angiopoietin-related protein, angiopoietin-related protein induces endothelial cell sprouting.";

J. Biol. Chem. 274:26523-26528(1999).

CC - FUNCTION: INDUCES SPROUTING IN ENDOTHELIAL CELLS THROUGH AN AUTOCRINE AND PARACRINE ACTION (BY SIMILARITY).

CC - SUBCELLULAR LOCATION: Secreted (By similarity).

CC - TISSUE SPECIFICITY: Widely expressed (By similarity). TONGUE, LUNG AND SKELETAL MUSCLE. ALSO FOUND IN LOWER LEVELS IN KIDNEY, EPIDIDYMUS AND TESTIS.

CC - SIMILARITY: Contains 1 fibrinogen C-terminal domain.

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CC -----

CC EMBL; AF125176; AAD55358.1; ..

CC HSSP; P02671; 1F2D.

CC VSD; MGI:347032; Angptl2.

CC InterPro; IPR002181; Fibrinogen C.

CC Pfam; PF00147; fibrinogen_C; 1.

CC SMART; SM00186; FBG; 1.

CC PROSITE; PS00514; FIBRIN AG C DOMAIN; 1.

CC Signal; Coiled coil; Glycoprotein.

CC SIGNAL 1 19 POTENTIAL.

CC CHAIN 20 493 ANGIOPOIETIN-RELATED PROTEIN 2.

CC DOMAIN 77 115 COILED COIL (POTENTIAL).

CC DOMAIN 152 202 COILED COIL (POTENTIAL).

CC DOMAIN 438 450 FIBRINOGEN C-TERMINAL.

CC DISULFID 278 337 BY SIMILARITY.

CC DISULFID 430 443 N-LINKED (GLCNAC...) (POTENTIAL).

CC CARBOHYD 164 164 N-LINKED (GLCNAC...) (POTENTIAL).

CC CARBOHYD 192 192 N-LINKED (GLCNAC...) (POTENTIAL).

CC SEQUENCE 493 AA; 57118 MW; 22885ABEF0746BF2 CRC64;

Query Match 20.4%; Score 485.5; DB 1; Length 493;

Best Local Similarity 30.8%; Pred. No. 1; 4e-25;

Matches 117; Conservative 62; Mismatches 128; Indels 73; Gaps 12;

QY 66 LQLPKQFSRISEVFKEV-----CNLKEIVNSLKKSCODCKLOADDNGCPGNSGLLPSTGA 121

DB 170 LQLASKYKDLERKFOHLAMLAHQSEVIAQLSEHCQV-----PAARVPQPP2AA 220

QY 122 PCEVGD---NSVRELESEVNLSELKNAKEEIVLHGRLEKJLVNKNNIENKVVDSKV 177

QY 221 PRRVQPTYNRI-----INGISTNEIQSDCKVLPSPSLPTN2AL----- 262

DB 178 ANLTVFNSLDGCKSCPKSQEQIQRPRVQHLYKDCSYVAIGKRSSETYRTPPFKSS 237

DB 262 -----TSLPSTKPSGP-----WRCLQALEGDHGSTSYLVKPKENTRL 302

QY 238 FEVYCDMETMGSGVTLQALDGSNFTFTWQYKAGFONJRRRWLGNKDKHLTKSKKE 297

DB 303 MGVWCQDRHDPGGWTVQRRLDGVSNNFRFMETVKGFGNIGEVWGLGENTYWLNGCN 362

QY 298 MTLRLIDLEPFGVELVALDQFVAKELKYLHGVNNGTAGDLPENKYNHDLKFFT 357

DB 363 YKLLVTNEDSGRKKVPAEYASTFLEPSEVYKRLIGFYHGNAGSFTV-----HNGKFT 417

QY 358 TPKDKNDYRPSGNGCLYSSGWNFDACLSSANLNGKYV---HQRVGRNIGFTWGTWGS 414

DB 418 TLDRDHDVY-TGNCAHYQKGGWYNACASNLTGYRSGHVESR-YQGVYWAERFG--- 473

QY 415 EAHPGGYKSKFKAKKQK1RP 434

DB 474 ----GSY--SLKKVVMWRP 487

RESULT 11

FIBS_HUMAN STANDARD; PAT; 453 AA.

AC P02679; P04469; P04470; Q96A14; Q96K23;

DT 21-JUL-1986 (Rel. 01, Created)

DT 29-FEB-2003 (Rel. 41, Last sequence update)

DT 15-SEP-2003 (Rel. 42, Last annotation update)

DE Fibrinogen gamma chain precursor (PRO2061).

GN FG3.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

OX NCBI_TaxID=9606;

RN [1]

RP SEQUENCE FROM N.A. (ISOFORMS GAMMA-A AND GAMMA-B).

RX MEDLINE=85252774; PubMed=2990550;

RA R-xon Y.W., Chung D.W., Davie E.W.;

RT "Nucleotide sequence of the gene for the gamma chain of human fibrinogen";

RT Biochemistry 24:2077-2086(1985).

RL [2]

RN SEQUENCE FROM N.A.

RP MEDLINE=83283434; PubMed=6688357;

RX Chung D.W., Chan W.-Y., Davie E.W.;

RA "Characterization of a complementary deoxyribonucleic acid coding for the gamma chain of human fibrinogen";

RT Biochemistry 22:3250-3256(1983).

RL [3]

RN SEQUENCE FROM N.A. (ISOFORMS GAMMA-A AND GAMMA-B).

RA Rieder M.J., Carrington D.P., Chung M.-W., Lee K.L., Poel C.L., Yi Q., Nickerson D.A.;

RA Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.

RL [4]

RP SEQUENCE FROM N.A. (ISOFORM GAMMA-A).

RC TISSUE=Fetal liver;

RA Zhang C., Yu Y., Zhang S., Wei H., Zhou G., Bi J., Zhang Y., Liu M., He F.;

RA "Functional prediction of the coding sequences of 33 new genes deduced by analysis of cDNA clones from human fetal liver";

RA Submitted (JAN-1999) to the EMBL/GenBank/DBJ databases.

RL [5]

RP SEQUENCE FROM N.A. (ISOFORM GAMMA-A).

RC TISSUE=Skeletal muscle;

RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D., Altshul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K., Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F., Diatchenko J., Marusina K., Farmer A.A., Rubin G.M., Hong L., Scapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E., Brownstein M.J., Udén T.B., Toshyuki S., Carninci P., Prange C., Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J., Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gutaratne P.H., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A., Whitting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Buetow K.H., White P., McEwan P.J., McKernan K.J., Malek J.A., Gutaratne P.H., Bhat N.K., Krzywinski M.I., Skalska J., Smalusz D.E., Schreier A., Schein J.E., Jones S.J.M., Marra M.A.;

RA "Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences";

RA Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).

RL [6]

RP SEQUENCE OF 27-437.

RA Henschel A., Lottspeich F., Southan C., Topfer-Petersen E.;

RT "Human fibrinogen: sequence, sulfur bridges, glycosylation and some structural variants.";

RL (in) Peeters H. (eds.);

RL Protides of the biological fluids, Proc. 28th colloquium, pp.51-56, Pergamon Press, Oxford (1980).

RL [7]

RT "Localization of a fibrin gamma-chain polymerization site within
 RL segment Thr-374 to Glu-396 of human fibrinogen.";
 RL Proc. Natl. Acad. Sci. U.S.A. 81:5980-5984(1984).
 [18] RN
 RP POLYMERIZATION SITE
 RX MEDLINE=81142375; Pubmed=6451630;
 RA Olexa S.A., Budzynski A.Z.;
 RL "Localization of a fibrin polymerization site.";
 RL J. Biol. Chem. 256:3544-3549(1981).
 [19] RN
 RP PLATELET AGGREGATION SITE
 RX MEDLINE=84203545; Pubmed=6326808;
 RA Kloczewiak M., Timmons S., Lukas T.J., Hawiger J.;
 RL "Platelet receptor recognition site on human fibrinogen. Synthesis
 RL and structure-function relationship of peptides corresponding to the
 RL carboxy-terminal segment of the gamma chain.";
 RL Biochemistry 23:1767-1774(1984).
 [20] RN
 RP PLATELET AGGREGATION SITE
 RX MEDLINE=84185664; Pubmed=6325435;
 RA Plow E.F., Stouffer A.H., Meyer D., Marguerie G., Ginsberg M.H.;
 RL "Evidence that three adhesive proteins interact with a common
 RL recognition site on activated platelets.";
 RL J. Biol. Chem. 259:5388-5391(1984).
 [21] RN
 RP CALCIUM-BINDING SITE
 RX MEDLINE=85261382; Pubmed=3160702;
 RA Dang C.V., Ebert R.F., Bell W.R.;
 RL "Localization of a fibrinogen calcium binding site between
 RL gamma-subunit positions 311 and 336 by terbium fluorescence.";
 RL J. Biol. Chem. 260:9713-9719(1985).
 [22] RN
 RP CHROMATOGRAPHIC COMPARISON OF GAMMA-A AND GAMMA-B CHAINS.
 RX MEDLINE=91054908; Pubmed=6933547;
 RA Wolfenstein-Tode C., Mosesson M.W.;
 RL "Human plasma fibrinogen heterogeneity: evidence for an extended
 RL carboxyl-terminal sequence in a normal gamma chain variant
 RL (gamma1).";
 RL Proc. Natl. Acad. Sci. U.S.A. 77:5069-5073(1980).
 [23] RN
 RP X-RAY CRYSTALLOGRAPHY (2.1 ANGSTROMS) OF 169-437.
 RX MEDLINE=97169449; Pubmed=3016719;
 RA Yee V.C., Pratt K.P., Cote H.C.F., le Trong I., Chung D.W.,
 RA Davie E.W., Stenkamp R.E., Teiller D.C.;
 RL "Crystal structure of a 30 kDa C-terminal fragment from the gamma
 RL chain of human fibrinogen.";
 RL Structure 5:125-138(1997).
 [24] RN
 RP X-RAY CRYSTALLOGRAPHY (2.1 ANGSTROMS) OF 169-437.
 RX MEDLINE=97352771; Pubmed=9207064;
 RA Pratt K.P., Cote H.C.F., Chung D.W., Stenkamp R.E., Davie E.W.;
 RL "The primary fibrin polymerization pocket: three-dimensional
 RL structure of a 30-kDa C-terminal gamma chain fragment complexed with
 RL the peptide Gly-Pro-Arg-Pro.";
 RL Proc. Natl. Acad. Sci. U.S.A. 94:7176-7181(1997).
 [25] RN

[illegible]

QY 188 DQKSKCSQEQIQSPFVQHLLYKDCSYAYALKBSSSEYTRVTPPKNSSEFVYCDMETX 247
 DB 158 EAQQCE-PCKDTVQ---IHDITGKQCDIANKGAKOSGLYFKPK:KAKQFLVYCEIDGS 213
 QY 248 GGGWTVLOARLDGSGTNEFTWQYKAGFNL---RRREFWLGNDKIHLLTJSKEV--ILR 301
 DB 214 GNGWTVFKRLDGSVDPKWQYKQYEGFGLSPTGTTTFWLGNEKIHLLISTCSA:PYALR 273
 QY 302 IDLEPNFNGVELYALYDQFYVANEFLKYLJHGVNY NGTAGDAL-RFNKHYKHDLKFFT-- 357
 DB 274 VELEDWNGRTSTADYAMPKVGEADKYLTYAFAGGAGDAGDFGDFGDDPSOKFFFTSH 333
 QY 358 -----TPKDKNDRPSGCGIYSSGKWFDACLSANLNGKYYH-----CKYRGVUNG 404
 DB 334 NGWQSTWQNDKFP-EGNCASQDGSQGWKXKCHAGHLNGVYQGYGTYSKASTPKGYDNG 392
 QY 405 IFWGTWMP-----GVSEA---HFGGVKSSFKKAKMIRPKH 436
 DB 393 --WA-WKTRWYSKTKTKMLIPNRLTIGEGQCHHGGK-----QVRPEH 438
 RESULT 12
 AGPI_MOUSE STANDARD; PRT; 498 AA.
 AC Q08538:
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Angiopoietin-1 precursor (ANG-1)
 GN AGPT1 OR AGPT
 OS Mus musculus (Mouse)
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 CX NCB:TaxID=10090;
 RN [1]
 RP MEDLINE=97134663; PubMed=8980223;
 RA Davis S., Adrich T.H., Jones P.F., Acheson A., Compton D.L., Jain V.,
 RA Ryan T.E., Bruno J., Radziejewski C., Maisorperle P.C.,
 RA Yancopoulos G.D.;
 RT "Isolation of angiopoietin-1, a ligand for the TIE2 receptor, by
 RT secretion-trap expression cloning";
 RL Cell 87:1161-1169(1996).
 CC -- FUNCTION: BINDS AND ACTIVATES TIE2 RECEPTOR BY INDUCING ITS
 CC TYROSINE PHOSPHORYLATION. IMPLICATED IN ENDOTHELIAL DEVELOPMENTAL
 CC PROCESSES LATER AND DISTINCT FROM THAT OF VEGF. APPEARS TO PLAY A
 CC CRUCIAL ROLE IN MEDIATING RECIPROCAL INTERACTIONS BETWEEN THE
 CC ENDOTHELIUM AND SURROUNDING MATRIX AND MESENCHYME. MEDIATES BLOOD
 CC VESSEL MATURATION/STABILITY. IT MAY PLAY AN IMPORTANT ROLE IN THE
 CC HEART EARLY DEVELOPMENT.
 CC -- SUBCELLULAR LOCATION: Secreted.
 CC -- DEVELOPMENTAL STAGE: EARLY IN DEVELOPMENT, AT E9 TO E11, IT IS
 CC FOUND MOST PROMINENTLY IN THE HEART MYOCARDIUM SURROUNDING THE
 CC ENDOCARDIUM. LATER, IT BECOMES MORE WIDELY DISTRIBUTED, MOST OFTEN
 CC IN THE MESENCHYME SURROUNDING DEVELOPING VESSELS, IN CLOSE
 CC ASSOCIATION WITH ENDOTHELIAL CELLS.
 CC -- SIMILARITY: Contains 1 fibronogen C-terminal domain.
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation
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 CC use by non-profit institutions as long as its content is in no way
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 CC or send an email to license@isb-sib.ch).
 DB EMBL: U83509; AAB50558.1;
 DB HSSP: P02671; 1F2D.
 DB XGD: MG1:208448; Agpt.
 DB GO: GO:0007169; P:transmembrane receptor protein tyrosine kin...; IDA.
 DB InterPro: IPR002181; Fibronogen_C.
 DB Pfam: PF00147; fibronogen_C_1.
 DB SMART: SM00186; FSG; 1.

DR PROSITE; PS00514; FIBRIN_AG_C_DOMAIN; 1.
 KW Angiogenesis; Glycoprotein; Coiled coil; Signal.
 FT SIGNAL 1 19
 FT CHAIN 20 498
 FT DOMAIN 81 119
 FT DOMAIN 153 261
 FT DOMAIN 284 498
 FT DISULFID 286 315
 FT DISULFID 439 452
 FT CARBOHYD 92 92
 FT CARBOHYD 122 122
 FT CARBOHYD 154 154
 FT CARBOHYD 243 243
 FT CARBOHYD 295 295
 SQ SEQUENCE 498 AA; 57505 MW; 28584FDEC26D800 CRC64;
 Query Match 20.3%; Score 483.5; DB 1; Length 498;
 Best Local Similarity 31.7%; Pred No. 1 9e-25;
 Matches 127; Conservative 62; Mismatches 141; Indels 71; Gaps 14;
 QY 61 LPLTLQLPKQFSRIE-----EVFKEYQNLKE:VNSLKKSCQCKLQADNGDNGPGRN 112
 DB 145 LTVETQVLNQTSLKLEQLLENSLSTYKLEKQLLQQTNEILKTHE-----KN 191
 QY 113 GLLLPSTGAPGVGNRVRESEVVKLSSELKNAXEE:NVLHGR-----LKNLVN 165
 DB 192 SLL-----EKKILEMEGKHEELDTLKEKENLQGLVSRQTFIIQZ:EK-QLSR 239
 QY 166 MNINIENVDSKANLTFVNSLQKSK-----CPSQEQIOSRPVQHLIYKDCSDYVAIGK 221
 DB 240 ATNNNSLQQLQQLMDTVNLVSLCTKGVLLKGGKREEKP-----PRCDADVYQAGF 294
 QY 222 RSSEYTRV---TPDPKNSSEFVYCDMETVGGWTVLQARLDGSGTNEFTWQYKAGFNG 277
 DB 295 NKSGIYTIYFNNEPEK---KVFQNDVNGGWTVIQHREDGSLDFQRCWKVEYKMGFGN 350
 QY 278 LRREFWLGNDKIHLLTJSKEVILRIDLEPNFNGVELYALYDQFYVANEFLKYLJHGVNYNG 337
 DB 351 PSGEYWLGNFEFFAITSQRYQYMLRIELMDWEGNRAYSQYDRPHIGNEKQNYRLYKGTG 410
 QY 338 TAGDALRFNKHYNHDLKFFTPDKNDRYPGSCG:YVSSGWMFADCLSANLNGKYYHQ- 396
 DB 411 TAGQSSLIH-GAD---FSTKADNDNCWC-KCALMTGGWAFDAGCPNSLNGMFTAG 465
 QY 397 KYRGVRNG:FWGTWPGVSEAHPGGYKSSFKKAKMIRPKHF 437
 DB 466 QNHGKLGINKHYFKGPS-----YSLRSTMTMIRPLDF 498
 RESULT 13
 ANL2_HUMAN STANDARD; PRT; 493 AA.
 AC Q9UKJ9;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Angiopoietin-related protein 2 precursor (Angiopoietin-like 2);
 GN ANGPTL2 OR ARP2.
 CS Homo sapiens (Human).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 CX NCB:TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Heart;
 RX MEDLINE=99403103; PubMed=10473614;
 RA Kim I., Moon S.-O., Koh K.N., Kim H., Uhm C.-S., Kwak H.J., Kim N.-G.,
 RA Koh G.Y.;
 RT "Molecular cloning, expression, and characterization of angiopoietin-
 RT related protein, angiopoietin-related protein induces endothelial ce-1
 RT sprouting";
 RL J. Biol. Chem. 274:26523-26528(1999).
 RN [2]


```
DR EMBL; M14773; AAA49261.1; ..
DR PIR; A25052; A25052.
DR PCB; IKWU; 23-AUG-02.
DR PCB; IKWU; 07-JAN-03.
DR InterPro; IPR002181; Fibrinogen_C.
DR SMART; SM00186; FBG; 1.
KW PROSITE; PS00514; FIBRIN AG C DOMAIN; 1.
FT Blood coagulation; Plasma; Sulfation; Glycoprotein; 3D-structure.
FT PEPTIDE 1 36
FT NCN_CONS 36 37
FT CHAIN <37 477 FIBRINOGEN BETA CHAIN.
FT MOD_RES 13 13 SULFATION.
FT CARBOHYD 27 27 N-LINKED (GLCNAC. .).
FT DISULFID 84 84 INTERCHAIN (WITH ALPHA CHAIN).
FT DISULFID 84 84 (BY SIMILARITY).
FT DISULFID 95 95 INTERCHAIN (WITH ALPHA CHAIN).
FT DISULFID 95 95 (BY SIMILARITY).
FT DISULFID 99 99 INTERCHAIN (WITH GAMMA CHAIN).
FT DISULFID 212 212 INTERCHAIN (WITH ALPHA CHAIN).
FT DISULFID 216 216 INTERCHAIN (WITH GAMMA CHAIN).
FT DISULFID 220 304 BY SIMILARITY.
FT DISULFID 230 259 BY SIMILARITY.
FT DISULFID 412 425 BY SIMILARITY.
SQ SEQUENCE 477 AA; 54270 MW; B8A95E7E3D09D18 CRC64;

Query Match 20.2%; Score 479.5; DB 1; Length 477;
Best Local Similarity 29.2%; Pred. No. 3.4e-25;
Matches 131; Conservative 66; Mismatches 138; Indels 113; Gaps 15;

QY 29 EIKDERAKVCPVRLSRCKCEAGECPQVSLPP;TQLPKQFRIEVEFVQNLRKEI 88
Db 100 EARELLKQDPVR-----YKISMLK-----CNLTYP 126
QY 99 VNSLKSCQCKLQADNDGDPGRNGLLPSTGAPGVGDNRVRELPSEVNVKLSSELQAK 148
Db 127 INSFDR-----MADSNLTQN-----VQTLARRLNSSSTHVNQ 162
QY 149 EFINVLHGRLEKLNLYMNMNIENVVDKVNLTFFVNSLGRCKSCK-----CPSEQEQTGRP 204
Db 163 KEI---ENAYKEVKI---RLESTVAGSLRSMKSVLEHJRAKXQRMEEAIKTKQELCSAP 215
QY 205 -----VQHLIYKCDPYAIGKRSSETVYVDPDPKNSFFCYCMETMGCKTVLQARL 256
Db 216 CTWCRCVPVSGMHCEDIYRNGRTSEAYIOPDLFSEPKYKFCDMESHGGGKTVVQNRV 275
QY 259 DGSNTFRTTQDYKAGFGNLR-----REFWLGNKDKHLTLTKKEMILRIDJEDF 307
Db 276 DGSSNFARDNTYKAFGNIAFGNGKSI CNIPCEYWLGT-KTVHQLTKQHTQVLFDMSDW 335
QY 308 NGVELYALYDQFVAVNEFLIKYRLHVNKNGTQGDAL-----RPNKHYN-HDLKFFET 358
Db 336 EGSSVYAQVAFSPENEAQGYRLWEDVSGNAGNALLEGATQAGSGNRTYTHNGMQEST 395
QY 359 PKCDNDRY-----PSGNGLYVSSGWWFEDCLSANLNGKYV-----HKQYGVNGFV 407
Db 396 FQNDNNMNPQDFTKHCSEDAGWVYNRCHAFNFRGYYWGG-VYTKQADYGTDDGVVN 455
QY 408 GTWPGVSEAHFGGYKXSFKEAKGVIRPK 435
Db 456 MNWKG-----SWY--SYRMAMKLRPK 475
```

RESULT 15

```
ID _AGE1_RAT
AC Q35420; O8K4Q4.
DT 16-OCT-2003 (Rel. 40, Created:
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Angiopoietin-1 precursor (ANG-1).
```

Query Match 19.9%; Score 473; DB 1; Length 497;
Best Local Similarity 30.1%; Pred. No. 9.7e-25;
Matches 125; Conservative 69; Mismatches 121; Indels 100; Gaps 16;

QY 61 LPPLTIQLPKQFSRIEVEFVQNLRKEIYNVS-----LKKSCQCKLQADNDGDPGRNG 113
Db 145 LTVETQVNLQTSRL-----EIQLLENSLSLYELEKQLQQTNEILKIQE-----KNS 192

GenCore version 5.1.6
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CM protein - protein search, using sw model

Run on: November 5, 2003, 16:37:23 : Search time 58.0176 Seconds
(without alignments)
1952.598 Million cell updates/sec

Title: US-09-902-563-2

Perfect score: 2378

Sequence: 1 MKLANNWLLSSAVLATYGF.....GYKSSPKERKMMTRPKRFPK 439

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 830525 seqs, 258052604 residues

Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: SP_TREMBL_23:*

2: sp_archaea:*

3: sp_bacteria:*

4: sp_fungi:*

5: sp_human:*

6: sp_invertebrate:*

7: sp_mammal:*

8: sp_mhc:*

9: sp_organelle:*

10: sp_plant:*

11: sp_rodent:*

12: sp_virus:*

13: sp_vertebrate:*

14: sp_unclassified:*

15: sp_virus:*

16: sp_bacteriophage:*

17: sp_archaea:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	2162.5	90.9	442	Q8MIP7	Q8MIP7 sus scrofa
2	1647	69.3	357	Q9EPT7	Q9EPT7 rattus norv
3	750	31.5	148	Q8WWE4	Q8WWE4 homo sapien
4	618.5	26.0	652	Q9KQD1	Q9KQD1 ciona intes
5	593.5	25.0	220	Q8T8A2	Q8T8A2 ciona savig
6	526	22.1	496	Q9C2D2	Q9C2D2 mus musculu
7	524	22.0	407	Q9CER1	Q9CER1 gallus gall
8	524	22.0	441	Q9DER0	Q9DER0 gallus gall
9	524	22.0	493	Q9DER0	Q9DER0 gallus gall
10	523	22.0	407	Q9PUS4	Q9PUS4 gallus gall
11	518.5	21.8	314	Q8VC25	Q8VC25 mus musculu
12	506	21.3	312	Q8MIP7	Q8MIP7 sus scrofa
13	505	21.2	491	Q9S841	Q9S841 homo sapien
14	496	20.9	244	Q9HBP3	Q9HBP3 homo sapien
15	491.5	20.7	513	Q90219	Q90219 brachydanio
16	491	20.6	337	Q8R1Q3	Q8R1Q3 mus musculu

17	489	20.6	346	4	Q43827	Q43827 homo sapien
18	485.5	20.4	292	5	Q9U8W8	Q9U8W8 tachypleus
19	485.5	20.4	493	11	Q8BX09	Q8BX09 mus musculu
20	483.5	20.3	498	11	Q8C2K6	Q8C2K6 mus musculu
21	482.5	20.3	488	13	Q91589	Q91589 xenopus lae
22	481.5	20.2	493	11	Q9J303	Q9J303 rattus norv
23	476	20.0	308	5	Q9U8M6	Q9U8M6 tachypleus
24	475	20.0	435	13	Q93568	Q93568 gallus gall
25	474.5	20.0	498	6	Q9BDY8	Q9BDY8 sus scrofa
26	473	19.9	489	13	Q9C2Z8	Q9C2Z8 brachydanio
27	471	19.8	316	5	Q9U8W7	Q9U8W7 tachypleus
28	460.5	19.4	461	4	Q8Y539	Q8Y539 homo sapien
29	456.5	19.2	324	5	Q95P99	Q95P99 halocynthia
30	456	19.2	341	5	Q956W1	Q956W1 halocynthia
31	456	19.2	481	11	Q8XGZ8	Q8XGZ8 mus musculu
32	455.5	19.2	236	4	Q8N2J9	Q8N2J9 homo sapien
33	454.5	19.1	431	6	Q95LU3	Q95LU3 macaca fasc
34	454	19.1	356	5	Q95P98	Q95P98 halocynthia
35	448	18.9	436	11	Q8VCM7	Q8VCM7 mus musculu
36	447.5	18.8	457	11	Q8R0Z6	Q8R0Z6 mus musculu
37	445.5	18.7	269	11	Q8BJE7	Q8BJE7 mus musculu
38	443.5	18.7	269	11	Q8BL54	Q8BL54 mus musculu
39	439.5	18.5	470	4	Q9BZZ0	Q9BZZ0 homo sapien
40	439.5	18.5	470	4	Q8NI99	Q8NI99 homo sapien
41	437	18.4	337	6	Q9BE00	Q9BE00 macaca fasc
42	435.5	18.3	235	6	Q28763	Q28763 papio cynoc
43	434.5	18.3	326	6	Q29042	Q29042 sus scrofa
44	434	18.3	200	11	Q8BMV1	Q8BMV1 mus musculu
45	433.5	18.2	324	5	Q95PA0	Q95PA0 halocynthia

ALIGNMENTS

RESULT 1

Q8MIP7	PRELIMINARY;	PRT;	442 AA.
AC	Q8MIP7		
DI	0-OCT-2002 (TrEMBLrel. 22, Created)		
DT	01-OCT-2002 (TrEMBLrel. 22, Last sequence update)		
DE	01-MAR-2003 (TrEMBLrel. 23, Last annotation update)		
DE	Fibrinogen-like protein 2.		
GN	FGL2		
OS	Sus scrofa (Pig).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.		
NC	NCBI_TaxID=9823;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RA	Chankar A, Liu H, Grant D.R., Levy G.A.		
RL	Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.		
DR	EMBL; AY112857; AAM52324.1; -		
DR	InterPro; IPR002181; Fibrinogen_C.		
DR	Pfam; PF00147; fibrinogen_C_1.		
DR	SMART; SM00186; FBG; 1.		
DR	PROSITE; PS00514; FIBRIN_AG_C_DOMAIN; 1.		
DR	SEQUENCE 442 AA; 50579 MW; 67800Da; 7AEDFF899 CRC64;		

Query Match.	Score 2162.5; DB 6; Length 442;
Best Local Similarity	59.1%; Pred. No. 8.5e-137;
Matches 392; Conservative	27; Mismatches 20; Indels 1; Gaps 1;
QY	1 MKLANNWLLSSAVLATYGFVANNKTEIKQRAKDVCPVLESRGKCEEGECPCYQVS 60
DB	3 LKLSNCKWLLSSAVLAAYGFLVANNKTEIKQRAKDVCPVLESRGKCEEGECPCYQVN 62
QY	61 LPPLTIQLPQPSRIEVEVKEVQNLKEIVNSLKSCQCKLQADNDGDPGRNGLLLPSTG 120
DB	63 LPPLTIQLPQPSRIEVEVKEVQNLKEIVNSLKSKTKQDRLQADNDGDPGRNGLLLPSTG 122
QY	121 APGEVDNRVRELESEVKNLSSELKNAKEEINVHGRLKLEKLVNMMNTENYVDSKVANL 180
DB	123 APGEADSRVRELESEVKNLSSELKNAKEEIDGLQGRLEKLSLVNMMNTENYVDSKVANL 182

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QY 181 TFVNSLDGKC-SKFSQSQIQRPVQHLYIKDCSDYVAIGKSSSEYVTPDPKNSFE 239
DB 183 TFVNSLDGKSSRCPSQBOIQSRPVQVHLYIKDCSEYVIGKSSSEYVTPDPKNSFE 242
QY 240 VYCDMETMGWTVLQARLDGSTNFTETWCYKAGFGLNRREFWLGNDKIHLLTKSKYI 299
DB 243 VYCDMETMGWTVLQARLDGSTNFTETWRDYKVGFGNLRREFWLGNDKIHLLTKSKYI 302
QY 300 LRIDLDGFNGVLYALYDQFYVANFLKYLRLHVGNNVINGTAGDALRPNKYNHDLKFFTP 359
DB 303 LRIDLDGFNGIKLYALYDHFYVANFLKYLRLHGVNNGTAGDALRFSKHYNEDKXFFTP 362
QY 360 DKNDRIYPSGNGCLYYSQGWFDACLSANLNGKYHQQYGVNRNIFWGTWPGVSEAHPG 419
DB 363 DRNDRIYPSGNGCLYYSQGWFDACLSANLNGKYHQQYGVNRNIFWGTWPGVSEAHPG 422
QY 420 GYKSSFKKAKMIRPKHXP 439
DB 423 GRSSFKKAKMIRPKHXP 442

RESULT 2
Q9EPT7 PRELIMINARY; PRT; 357 AA.
AC Q9EPT7;
DT 01-MAR-2001 (TrEMBLrel. 16, Created);
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update);
DE Prcthrioninase FG2.
CS Rattus norvegicus (rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
CX NCBI_TaxID=10116;
RN [1]
RP STRAIN=Sprague-Dawley;
RC Rychlik D F, Chien E, Phillippe M.;
RT "FG2 Expression in the Sprague-Dawley Rat.";
RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF323608; AAG42269.1; -.
DR HSSP; P02671; 1P2D.
DR InterPro; IPR002181; Fibrinogen_C.
DR Pfam; PF00147; fibrinogen_C.
DR SMART; SM00186; FBG; 1.
DR PROSITE; PS00514; FIBRIN_AG_C_DOMAIN; 1.
SQ SEQUENCE 357 AA; 40966 MW; 31183D9A02E5BA9 CRC64;

Query Match 69.3%; Score 1647; DB 11; Length 357;
Best Local Similarity 82.7%; Pred. No. 2e-102;
Matches 302; Conservative 24; Mismatches 31; Indels 8; Gaps 1;

QY 75 IBEVFEVONLKEIVNSLKKSCQCKLQADNGDPPGNGLLLPSTCAPGFGVGNVRELE 134
DB 1 MEEVLKEVRLTQEAVDLSLKKSCQCKLQADNPFDPGNG-----AETAEDNRVQBLE 52
QY 135 SEVYKLSSEKNAKESINVLHGLEKLNLVNNENYVDSKVANLTFVNSLSDGCKSKC 194
DB 53 SYNVKLSSEKNAKESIQGLQGLRSLQVKNXNIENYVDKVNKLSVNSLSDSKCFKC 112
QY 195 PSQEQSQSRPVQVHLYIKDCSDYVAIGKSSSEYVTPDPKNSSEFYVCDNETMGWTVL 254
DB 113 PSQEHQNPVQVHLYIKDCSDYVVLKRSSTVTPDPHNSSEFYVCDNETTGGWTVL 172
QY 255 QARLDGSTNFTRWQDYKAGFGLNRREFWLGNDKIHLLTKSKEMILRLDLEFNGVLYIA 314
DB 173 QARLDGSTNFTRWQDYKAGFGLNRREFWLGNDKIHLLTKSKEMILRLDLEFNGVLYIA 232
QY 315 LYDQFYVANFLKYLRLHVGNNVINGTAGDALRPNKYNHDLKFFTPDKNDRIYPSGNGCLY 374
DB 233 YDQFYVANFLKYLRLHVGNNVINGTAGDALRFSRHHYHDLRFFTPDRNDRIYPSGNGCLY 292
QY 375 YSSGWFDACLSANLNGKYHQQYGVNRNIFWGTWPGVSEAHPGSKSFKEAKMIRP 434
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DB 293 YSSGWFDACLSANLNGKYHQQYGVNRNIFWGTWPGVSEAHPGSKSFKEAKMIRP 352
QY 435 KXFKP 439
DB 353 KXFKP 357

RESULT 3
Q8WWE4 PRELIMINARY; PRT; 148 AA.
AC Q8WWE4;
DT 01-MAR-2002 (TrEMBLrel. 20, Created);
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update);
DE C-OCT-2002 (TrEMBLrel. 22, Last annotation update);
DE Similar to fibrinogen-like 2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
CX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Lung;
RA Strausberg R.;
RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC017813; AAH17813.1; -.
SQ SEQUENCE 148 AA; 16561 MW; 456B7DBA37CC7F21 CRC64;

Query Match 31.5%; Score 750; DB 4; Length 148;
Best Local Similarity 99.3%; Pred. No. 7.1e-43;
Matches 144; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 XKLAWYMLSSAVLYATYGFLLVANNETEEIKDPRANDVCPVRLESRGKCEAGCCPYQVS 60
DB 1 XKLAWYMLSSAVLYATYGFLLVANNETEEIKDPRANDVCPVRLESRGKCEAGCCPYQVS 60
QY 61 LPPLTICLPKQFSRIBEVFEVONLKEIVNSLKKSCQCKLQADNGDPPGNGLLLPSTG 120
DB 61 LPPLTICLPKQFSRIBEVFEVONLKEIVNSLKKSCQCKLQADNGDPPGNGLLLPSTG 120
QY 121 APGEVGNRVRELESEVNSLSELK 145
DB 121 APGEVGNRVRELESEVNSLSELK 145

RESULT 4
Q9NDQ1 PRELIMINARY; PRT; 652 AA.
AC Q9NDQ1;
DT 01-OCT-2000 (TrEMBLrel. 15, Created);
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update);
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update);
DE Fibrinogen-like protein.
GN CI-FIBRN.
OS Ciona intestinalis.
OC Eukaryota; Metazoa; Chordata; Urochordata; Ascidiacea; Enterogena;
OC Phlebobranchia; Cionidae; Ciona.
CX NCBI_TaxID=7719;
RN [1]
RP SEQUENCE FROM N.A.
RA Hotta K., Takahashi H., Asakura T., Saitoh B., Takatori N., Satou Y.,
RA Satoh N.;
RT "Characterization of Brachyury downstream notochord genes in the Ciona
intestinalis embryo.";
RL Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB036849; BABCC626.1; -.
DR HSSP; P02671; 1P2D.
DR InterPro; IPR002181; Fibrinogen_C.
DR Pfam; PF00147; fibrinogen_C.
DR SMART; SM00186; FBG; 1.
DR PROSITE; PS00514; FIBRIN_AG_C_DOMAIN; 1.
SQ SEQUENCE 652 AA; 73252 MW; A492BA325162F0EC CRC64;
```

Query Match	26.0%	Score 610.5	DB 5	Length 652
Best Local Similarity	43.0%	Pred. No. 2.9e-33		
Matches 120	Conservative 53	Mismatches 91	Indels 15	Gaps 6

QY	171	NVYDSKVANLT-----FVNVLGG-----KSKKCPSEQIQSRPQHLYIKDCSDYYATGK	221
DB	371	NVYSEGSGWNRDGYATNETEGHEFTSRIRATNPFPVODGGTSECPY-DCRELYARGV	429
QY	222	RSSEYRVTPDPKNSFEVYCDMETMGAGWTVLQARLDGSTNFRTWQDYKAGFKNLRRE	281
DB	430	RCGSGVYDIPGPK-VTVTVYCDMTDGGWMTL-CRRIDGIVNFSKCKSKYKSGFGDINAD	488
QY	282	FWLGNCKLHLLT---KSKEMLRILDJDFNGVELYALYDCFYVANFLKYRLJHVNNGYT	339
DB	489	HWIGLEKHHISTNSKSRMELRLNTCDWDSHYANYGVIRSESGKYQLIAKEYTGT	548
QY	339	AGDALREKHNHDLKFFTFTECKNDYRPSGNCGLYVSSGWMFACL SANLNGKYTHCKY	398
DB	549	AGDALNYGENYHHLQPTTFTERNDGYALNGCRYYRSGWENACFAALNNGNYTTFY	608
QY	399	RGVRNGIFWGTWPGVSEAHPGGYKSSFKKAMMRPKHF	437
DB	609	KGVQNGYKNGTWYK-LSDS-TSKSRYSFKYVDMKVRPLNF	646

RESULT 5	
Q8T8A2	
CD	C9T8A2 PRELIMINARY; PRT; 220 AA.
AC	C9T8A2;
DT	01-JUN-2002 (TrEMBLrel. 21, Created)
DT	01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT	01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE	Fibrinogen-like protein (Fragment).
DE	Fibrinogen-like protein (Fragment).
GN	CS-FIBRINOGEN-LIKE.
OS	Ciona savignyi.
OC	Eukaryota; Metazoa; Chordata; Urochordata; Ascidiacea; Enterogona;
OC	Phlebobranchia; Cionidae; Ciona.
OX	NCBI_TaxID:51511;
RN	[1]
RP	SEQUENCE FROM N.A.
RX	MEDLINE=21920613; PubMed=11923208;
RA	Imai K.S., Satch N., Sato Y.;
RT	"Early embryonic expression of FGF4/6/9 gene and its role in the induction of mesenchyme and notochord in Ciona savignyi embryos.";
RL	Development 129:1729-1738(2002).
DR	EMBL; AB073373; BAB88674.1; .
DR	InterPro; IPR002181; Fibrinogen_C.
DR	InterPro; PF00147; Fibrinogen_C.1.
DR	SMART; SM00186; FBG; 1
DR	PROSITE; PSC0514; FIBRIN_AG_C_DOMAIN; 1.
FT	NON_TER
FT	1
SQ	SEQUENCE 220 AA; 25758 MW; 4160FAE727F3ED06 CRC64;

Query Match	25.0%	Score 593.5	DB 5	Length 220
Best Local Similarity	49.8%	Pred. No. 3.5e-32		
Matches 107	Conservative 42	Mismatches 61	Indels 5	Gaps 3

QY	227	YVITDPKNSFEVYCDMETMGAGWTVLQARLDGSTNFRTWQDYKAGFKNLRSEFLGN	286
DB	4	YEIKEN-TDETVVYCDNETAGGTVTIQRVZGEENFSGNKKAYKNGFGDKKDKWIGL	62
QY	287	DKIHLLT---KSKEMLRILDJDFNGVELYALYDCFYVANFLKYRLJHVNNGYTAGDAL	343
DB	63	ERWHLLTTSNKSRRKLRLDLDWDDVHVVAVEVTFVRGEGNYGLIAKKSFTAGDAL	122
QY	344	RFNGYHNHDLKFFTFTECKNDYRPSGNCGLYVSSGWMFACL SANLNGKYTHCKYGRN	403
DB	123	NYGENYENHQAFTTFDRDNDGYALNGCRYYRSGWENACFAALNNGNYTTFYRGVN	182
QY	404	GIFWGTWPGVSEAHPGGYKSSFKKAMMRPKHF	439
DB	183	GIYWGTVWKLSDRSNA-RYSFKYVDMKVRPLNF	216

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RESULT 6
Q9D2C2 Q9D2C2 PRELIMINARY; PRT; 496 AA.
AC C9D2C2;
CT 01-JUN-2001 (TReMBUrel. 17, Created)
CT 01-JUN-2001 (TReMBUrel. 17, Last sequence update)
DT 01-MAR-2003 (TReMBUrel. 23, Last annotation update)
DE 1c-dar pregnant adult female ovary and uterus cDNA, RIKEN full-length
DE enriched library, clone:5031400218, full insert sequence (Angiopoietin
DE 2).
DE AGPT2.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
CX NCBI_TaxID=10090;
RN [1]
RE SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Ovary, and Uterus;
RX MEDLINE=21698566; PubMed1127851;
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Aizawa K., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Arakawa K., Iwama M., Nishi K., Kiyosawa H., Kondo S., Yananaka I.,
RA Saico T., Okazaki Y., Gotohori T., Bono H., Kasukawa T., Saico R.,
RA Kagota K., Matsuda H.A., Asahburner M., Batalov S., Casavant T.,
RA Fleisemann W., Gaasterland T., Gissi C., King B., Koshiwa H.,
RA Klei P., Lewis S., Matsuy P., Nikaido I., Pesole G., Quackenbush J.,
RA Schriml J.M., Stauffer P., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Saka K., Okido T., Fururo M., Aono H., Baldarelli R., Barsh G.,
RA Blake K., Boiffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gusmanich S., Hill D., Hofmann M., Hure D.A., Kamiya Y., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli C., Mombaerts P.,
RA Norcone P., Ning B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawai H., Kohsaki S.,
RA Hayashizaki Y.;
RA "functional annotation of a full-length mouse cDNA collection.";
RA Nature 409:685-690(2001).
RJ [2]
RN SEQUENCE FROM N.A.
RL Strausberg R.;
RN Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
RN [3]
RN SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Head;
RX MEDLINE=22354683; PubMed=12466851;
RA The FANTOM Consortium,
RA "The RIKEN Genome Exploration Research Group Phase I & II Team;
RA "Analysis of the mouse transcriptome based on functional annotation of
RA 60,770 full-length cDNAs.";
RL Nature 420:563-573(2002).
RL EMBL; AK019860; BAB31887.1;
RL EMBL; BC027216; AAC27216.1;
RL EMBL; AKC48622; BAC33396.1;
RL HSP; P02671.1; P2D.
DR MGD; MGI:1202890; Agpt2.
DR InterPro; IPR002181; Fibrinogen_C.
DR Pfam; PF00147; fibrinogen_C; 1.
DR SMART; SM00186; FBG; 1.
DR PROSITE; PS00514; FIBRIN_AG_C_DOMAIN; 1.
DR SEQUENCE 496 AA; 56575 MW; E7563B498A0EF331 CRC64;
Query Match 22.1%; Score 526; DB 11; Length 496;
Best Loca. Similarity 32.9%; Pred. No. 3.2e-27;
Matches 127; Conservative 66; Mismatches 153; Indels 40; Gaps 9;
QY 61 LPPLTQLPKQFSRIEVEFKVEYONLKEIVNSLKSCODCKLOADNGDGRNGLLPSTG 123
DB 142 LTDVEAQVLNQTLRT-----ELQLQHSISTNKLKQLDQTSE-NKLGNKNRFL----- 191
QY 121 APGEVGNRVRREIESEYVKN-SSELKKAKEINVLHGRL-----EKLVNMMNIENY 172

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Db 192 -----EQKVLMEGSHSEQLQKMEKQDEHGLVLSKQSSVIDEERKLVATVNN--SL 243
Qy 173 VDSKVANLTFVNSJLGGKSKCPSQFOIGSRPVCHLVKDCSDYVAIGKSSSETVAV--PD 232
Db 244 LKQKQHLMETVNSLLTMSSSNSKSSVAIRKEEQTTFRDCAEIPKSLTSGIYTLTFP 303
Qy 233 PKNSFEVYCDMETGGWTVLQARLDGSTNFTRTWQDYKAGFNLRRFWLGNCKIHLL 292
Db 304 NSTEELKAYCDMEVGGGWTVLQRRDGSVDQRTWKEYKEGFGSLGEYWLGNFVSQ 363
Qy 293 TKSKEMLRIDLEDFNGVELYALYDOFYVANFELKYLHVGNVNGTAGDALRFNKHYND 352
Db 364 TQCHRYVLKIQKMEGNEFAHSLYDHFYLAGESNYRHLTCTGTAGKISS--SQFGSD- 422
Qy 353 LKFFTPDKNDRYPSGNCGLYSSGWFDACLSANLNGKYHQYKRGVR-NGIPFWGTP 411
Db 423 ---FSTKSDNDKIC-KCSQMLSGGWFDA CGPSNKGNGYYPQKQNTKNGIKWYYK 478
Qy 412 GVSEAHPPGGYKSKFKAQKMIKPKHF 437
Db 479 G-----SGY--SLKATTMMIRPADF 496

RESULT 7
QORDER1 PRELIMINARY; PRT; 407 AA.
AC QORDER1
D 01-MAR-2001 (TREMELrel. 16, Created)
D 01-MAR-2001 (TREMELrel. 16, Last sequence update)
D 01-DEC-2001 (TREMELrel. 19, Last annotation update)
DE Angiopoietin-2B.
GN ANGIOPOIETIN-2B.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20422311; PubMed=10964717;
RA Mezquita J., Mezquita P., Montserrat P., Mezquita B., Francane V.,
RA Vilagrasa X., Mezquita C.;
RT "Genomic structure and alternative splicing of chicken angiopoietin-
RT 2";
RL Biochem. Biophys. Res. Commun. 275:643-651(2000).
DR EMBL; AJ289778; CAC08175.1; -.
DR HSP; P02671; IFLD.
DR InterPro; IPR002181; Fibrinogen_C.
DR Pfam; PF00147; fibrinogen_C; 1.
DR SMART; SM00186; FBG; 1.
DR PROSITE; PS00514; FIBRIN_AG_C_DOMAIN; 1.
SQ SEQUENCE 407 AA; 46687 MW; 8963BA0AB8C7A41C CRC64;

Query Match 28.0%; Score 524; DB 13; Length 407;
Best Local Similarity 38.3%; Pred. No. 3.4e-27;
Matches 125; Conservative 45; Mismatches 120; Indels 36; Gaps 10;

Qy 127 DNRVRESEVKNLSSELKNAKEENVLHGR-----LEK-LNLVNMNI-----ENYV 173
Db 103 EKRVLMEDEKHTLQLKSIKDEKDLQVLVARQNSIIELEKQLVATVNNSVLQKQOHD 162
Qy 174 DSKVAN-LTFVNSJLGGKSKCPSQFOIGSRPVCHLVKDCSDYVAIGKSSSETVAVTPD 232
Db 163 METVHLLTWISTPNSAKNFTAKEEQIS-----FKDCAEAFKSLTSGIYTLTFP 214
Qy 233 PKNSFEVYCDMETGGWTVLQARLDGSTNFTRTWQDYKAGFNLRRFEFLGNCKIHLL 292
Db 215 NSAQEKKAYCDMESNGGWTVLQRRDGSVDHRTWKEYKIGFGDPAGEYWLGNFVSQ 274
Qy 293 TKSKEMLRIDLEDFNGVELYALYDOFYVANFELKYLHVGNVNGTAGDALRFNKHYND 352
Db 275 TNOKRYVLKILKDWEGNEAYTLYDQFYLANBEQYRIHLKGLTGTAGKISSISQPGND- 333

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Qy 353 LKFFTPDKNDRYPSGNCGLYSSGWFDACLSANLNGKYHQYKRGVR-NGIPFWGTP 411
Db 334 ---FSTKSDNDKIC-KCSQMLTGGWFDA CGPSNKGNGYYPQKQNTKNGIKWYYK 389
Qy 412 GVSEAHPPGGYKSKFKAQKMIKPKHF 437
Db 390 G-----SGY--SLKATTMMIRPADF 407

RESULT 8
QORDER0 PRELIMINARY; PRT; 441 AA.
AC QORDER0
D 01-MAR-2001 (TREMELrel. 16, Created)
D 01-MAR-2001 (TREMELrel. 16, Last sequence update)
D 01-DEC-2001 (TREMELrel. 19, Last annotation update)
DE Angiopoietin-2C.
GN ANGIOPOIETIN-2C.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20422311; PubMed=10964717;
RA Mezquita J., Mezquita P., Montserrat P., Mezquita B., Francane V.,
RA Vilagrasa X., Mezquita C.;
RT "Genomic structure and alternative splicing of chicken angiopoietin-
RT 2";
RL Biochem. Biophys. Res. Commun. 275:643-651(2000).
DR EMBL; AJ289779; CAC08176.1; -.
DR HSP; P02671; IFLD.
DR InterPro; IPR002181; Fibrinogen_C.
DR Pfam; PF00147; fibrinogen_C; 1.
DR SMART; SM00186; FBG; 1.
DR PROSITE; PS00514; FIBRIN_AG_C_DOMAIN; 1.
SQ SEQUENCE 441 AA; 50472 MW; DC98127FE0CE34E2 CRC64;

Query Match 22.0%; Score 524; DB 13; Length 441;
Best Local Similarity 38.3%; Pred. No. 3.8e-27;
Matches 125; Conservative 45; Mismatches 120; Indels 36; Gaps 10;

Qy 127 DNRVRESEVKNLSSELKNAKEENVLHGR-----LEK-LNLVNMNI-----ENYV 173
Db 137 EKRVLMEDEKHTLQLKSIKDEKDLQVLVARQNSIIELEKQLVATVNNSVLQKQOHD 196
Qy 174 DSKVAN-LTFVNSJLGGKSKCPSQFOIGSRPVCHLVKDCSDYVAIGKSSSETVAVTPD 232
Db 197 METVHLLTWISTPNSAKNFTAKEEQIS-----FKDCAEAFKSLTSGIYTLTFP 248
Qy 233 PKNSFEVYCDMETGGWTVLQARLDGSTNFTRTWQDYKAGFNLRRFEFLGNCKIHLL 292
Db 249 NSAQEKKAYCDMESNGGWTVLQRRDGSVDHRTWKEYKIGFGDPAGEYWLGNFVSQ 308
Qy 293 TKSKEMLRIDLEDFNGVELYALYDOFYVANFELKYLHVGNVNGTAGDALRFNKHYND 352
Db 309 TNOKRYVLKILKDWEGNEAYTLYDQFYLANBEQYRIHLKGLTGTAGKISSISQPGND- 367
Qy 353 LKFFTPDKNDRYPSGNCGLYSSGWFDACLSANLNGKYHQYKRGVR-NGIPFWGTP 411
Db 368 ---FSTKSDNDKIC-KCSQMLTGGWFDA CGPSNKGNGYYPQKQNTKNGIKWYYK 423
Qy 412 GVSEAHPPGGYKSKFKAQKMIKPKHF 437
Db 424 G-----SGY--SLKATTMMIRPADF 441

RESULT 9
QORDER2 PRELIMINARY; PRT; 493 AA.
AC QORDER2

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DT C1-MAR-2001 (TRENBLrel. 16, Created)
DT 01-MAR-2001 (TRENBLrel. 16, Last sequence update)
DT 01-DEC-2001 (TRENBLrel. 19, Last annotation update)
DE Angiopoietin-2A.
GV ANGIOPOIETIN-2.
CS Gallus gallus (Chicken)
CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
CX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20422311; PubMed=10564717;
RA Mezquita J., Mezquita P., Montserrat P., Mezquita B., Francone V.,
RT Vilagrasa X., Mezquita C.;
RA "Genomic structure and alternative splicing of chicken angiopoietin-
RT 2."
RL Biochem. Biophys. Res. Commun. 275:643-651(2000).
DR EMBL; AJ285777; CAC08174.1; -.
DR HSSP; P02671; 1F2D.
DR InterPro; IPR002181; Fibrinogen_C.
DR Pfam; PF00147; fibrinogen_C; 1.
DR SMART; SM00186; FBG; 1.
DR PROSITE; PS00514; FIBRIN_AG_C_DOMAIN; 1.
DR SEQUENCE 493 AA; 56333 MW; BD421P9017256DA CRC64;
SQ
Query Match 22.0%; Score 524; DB 13; Length 493;
Best Local Similarity 38.3%; Pred. No. 4.3e-27;
Matches 125; Conservative 45; Mismatches 120; Indels 36; Gaps 10;

QY 127 DNEVRELESVNKLSEELKNAKEEINVLR-----LEK-LNLVNMMNI-----ENVV 173
Db 189 EKVLEMEDEKHTLOLQKSIKDEKQQLQVLRQNSIIELEKQLVTATVNSVLQKQCHL 248
QY 174 DSKVAN-LTFVNSLDGKCKSPSQEQISRPVQHLVYKDCSDYVYAIKRSSEYRVTPD 232
Db 249 METVHLLTWTSPNSAKNPF--AKEQIS-----FKQCAEAFKSLTSGYTLTFP 300
QY 233 PKNSSEFVYCDMETMGGWTVLQARLDGSTNFTWQDYKAGFNLRRFNLGNDKIHL 292
Db 301 NSAQEKKAYCMNESGGWTVLQRRDGSVDVHRTWKEVYKIGFGDPAGEYWLGNFVSQ 360
QY 293 TSKKEMILRIDLEDFNGVELYALYDQFYVANEFLKYRLHVGNNGTAGDALRFNKHYND 352
Db 361 TNQKRYVLKILKDWEGNEAYTLVQFYLANBEQKYRIHLKGLTGTAGKSSISQPGND- 419
QY 353 LKFFTPDKNDRYPSGNCGLYSSGWWFDCLSANLNGKYVHQYRGVVR-NGIFWGTWP 411
Db 420 ----FSTKADNDKIC-KCSQMLTGGWTFDAGCPNLNGMYYPRLQNNKFKGIKYYWK 475
QY 412 GVSEAHFGGYKSKFKEAKNMIRPKHF 437
Db 476 G-----SGY--SLKATTWVIRPADF 493

RESULT 13
Q9PJ54 PRELIMINARY; PRT; 407 AA.
ID Q9PU54;
AC Q9PU54;
DT 01-MAY-2000 (TRENBLrel. 13, Created)
DT 01-MAY-2000 (TRENBLrel. 13, Last sequence update)
DT 01-JUN-2001 (TRENBLrel. 17, Last annotation update)
DE Angiopoietin-2B (Ang-2B).
GV ANGIOPOIETIN-2.
CS Gallus gallus (Chicken)
CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
CX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=Hubbard White Mountain;
RX MEDLINE=99333704; PubMed=10403795;

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RA Mezquita J., Mezquita B., Pau M., Mezquita C.;
RT "Characterization of a novel form of angiopoietin-2 (Ang-2B) and
RT expression of VEGF and angiopoietin-2 during chicken testicular
RT development and regression."
RL Biochem. Biophys. Res. Commun. 260:492-498(1999).
DR EMBL; AJ131923; CAB59200.1; -.
DR HSSP; P02671; 1F2D.
DR InterPro; IPR002181; Fibrinogen_C.
DR Pfam; PF00147; fibrinogen_C; 1.
DR SMART; SM00186; FBG; 1.
DR PROSITE; PS00514; FIBRIN_AG_C_DOMAIN; 1.
DR SEQUENCE 407 AA; 45647 MW; E10C03D07E410013 CRC64;
SQ
Query Match 22.0%; Score 523; DB 13; Length 407;
Best Local Similarity 38.3%; Pred. No. 4e-27;
Matches 125; Conservative 45; Mismatches 120; Indels 36; Gaps 10;

QY 127 DNEVRELESVNKLSEELKNAKEEINVLR-----LEK-LNLVNMMNI-----ENVV 173
Db 103 EKVLEMEDEKHTLOLQKSIKDEKQQLQVLRQNSIIELEKQLVTATVNSVLQKQCHL 162
QY 174 DSKVAN-LTFVNSLDGKCKSPSQEQISRPVQHLVYKDCSDYVYAIKRSSEYRVTPD 232
Db 163 METVHLLTWTSPNSAKNPF--AKEQIS-----FKQCAEAFKSLTSGYTLTFP 214
QY 233 PKNSSEFVYCDMETMGGWTVLQARLDGSTNFTWQDYKAGFNLRRFNLGNDKIHL 292
Db 215 NSAQEKKAYCMNESGGWTVLQRRDGSVDVHRTWKEVYKIGFGDPAGEYWLGNFVSQ 274
QY 293 TSKKEMILRIDLEDFNGVELYALYDQFYVANEFLKYRLHVGNNGTAGDALRFNKHYND 352
Db 275 TNQKRYVLKILKDWEGNEAYTLVQFYLANBEQKYRIHLKGLTGTAGKSSISQPGND- 333
QY 353 LKFFTPDKNDRYPSGNCGLYSSGWWFDCLSANLNGKYVHQYRGVVR-NGIFWGTWP 411
Db 334 ----FSTKADNDKIC-KCSQMLTGGWTFDAGCPNLNGMYYPRLQNNKFKGIKYYWK 389
QY 412 GVSEAHFGGYKSKFKEAKNMIRPKHF 437
Db 390 G-----SGY--SLKATTWVIRPADF 407

RESULT 11
Q8VC25 PRELIMINARY; PRT; 314 AA.
ID Q8VC25;
AC Q8VC25;
DT 01-MAR-2002 (TRENBLrel. 20, Created)
DT 01-MAR-2002 (TRENBLrel. 20, Last sequence update)
DT 01-OCT-2002 (TRENBLrel. 22, Last annotation update)
DE Similar to fibrinogen-like 1.
GV FBJ.
OS Mus musculus (Mouse).
CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
CX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RA Strausberg R.;
RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC021946; AAH21946.1; -.
DR MGS; XGI:02795; Fg11
DR InterPro; IPR002181; Fibrinogen_C.
DR Pfam; PF00147; fibrinogen_C; 1.
DR SMART; SM00186; FBG; 1.
DR PROSITE; PS00514; FIBRIN_AG_C_DOMAIN; 1.
DR SEQUENCE 314 AA; 36439 MW; 52C16CA9C2D0386A CRC64;
SQ
Query Match 21.8%; Score 518.5; DB 11; Length 314;
Best Local Similarity 37.0%; Pred. No. 5.7e-27;
Matches 126; Conservative 42; Mismatches 116; Indels 57; Gaps 12;

QY 110 GRNCJJLPSTGAPCEVDNRVRELESEVNKLSEELKNAKEEINVLR-----LEK-LNLVNMMNI-----ENVV 168

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Db 17 GREGNALESCLRE-----CVR--RAQVQVETRVKQQTMIQLHEK--EVGFLEKGS 69
QY 169 :ENYVDSKVAANLTFVYNSLDKCKSPCEQIQSRPVQHLIYKDCSDYVYAIKRSSEIYR 228
Db 70 ENSFID-----LGGRQ-----YADCSEIYNDGFQCSGEYK 100
QY 229 VTPDPKNSSEFVYCDMETWGGWTVLQARLDGSIINFTTWQDYKAGPGLN---RRFPWLG 285
Db 131 IKPLQSLAEFVYCDMSD--GGGWTVIQRSDGSENFNRGMDYENGFGNFQVQNGEYKLG 159
QY 286 NDKHLLTKSKEMILRIDLEPFGVELYALYDQFYVANEFLKYR--HGVNYNGTAGDARLF 345
Db 160 KXNINLLT:QGYTLKIDLTDFEKNSFAQYQSFVKGDKKFFELNIGEYSGTAGDLSLG 219
QY 346 NKH-----YHDLKFFTPDKNDNDYPSGNGLYSSGKMPFADCLSANLNGKYHYKRYR 399
Db 220 TFHPEVQWASHQWKSTWDORDNRY--QGNCAEEEQSGWAFNRCHSANLNGVYRGSYR 276
QY 400 G-VRNGIPIWGTWPGVSEAHPGGYSKSFKEAKMMIRPKFKP 439
Db 279 AETDNGVWYWTM-----HGMWYSLKSVVVKIRPDSFIP 311

RESULT 12
QBNG32 PRELIMINARY; PRT; 312 AA.
AC QBNG32;
DT 01-OCT-2002 (TREMBLrel. 22, Created)
DT 01-OCT-2002 (TREMBLrel. 22, Last sequence update)
DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update);
DE LFIRE1.
GN LFIRE1.
CS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RA Yan J., Xu Y., Wang N., Xu Y.;
RT "LFIRE-1, a liver-specific expressing gene on human chromosome 8p22,
RT is frequently down-regulated and functions as tumor suppressor in
RT human hepatocellular carcinoma.";
PI Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
CR ENBL; AF168954; AAY86911.1; -.
DR InterPro; IPR002181; Fibrinogen_C.
DR Pfam; PF00147; fibrinogen_C; 1.
DR SMART; SM00186; FBG; 1.
DR PROSITE; PS00514; FIBRIN_AG_C_DOMAIN; 1.
SQ SEQUENCE 312 AA, 36377 MD, 7330F3D55A3CB619 CRC64;

Query Match 21.3%; Score 506; DB 4; Length 312;
Best Local Similarity 44.6%; Pred. No. 3.9e-26;
Matches 107; Conservative 25; Mismatches 89; Indels 20; Gaps 6;

QY 210 YKDCSYAIGKRSSEIYRVPDPKNSSEFVYCDMETWGGWTVLQARLDGSIINFTTWQ 269
Db 80 YADCSEIYNDGYSKGFQKIRPLQSPAEFVYCDMSD--GGGWTVIQRSDGSENFNRGK 138
QY 270 DYKAGFGLN---RRREFLGNQKIHLLTKSKEMILRIDLEPFGVELYALYDQFYVANEFL 326
Db 139 DYENGFGNFVQKHGEYVGLGNKLNHLFTTQEDYTLKIDLADEKISRVAQYKQFVGDEKN 198
QY 327 KYRJVHGVNYNGTAGDARFNKH-----YHDLKFFTPDKNDNDYPSGNGLYSSGWW 380
Db 199 FYELNIGEYSGTAGDSLGNHFEPCWASHQRMKFTWDRDHDNY--EGNCAEEDQSGW 257
QY 381 FDACLSANLNGKYHYKRYR--VRNGIFWGTWPGVSEAHPGGYSKSFKEAKMMIRPKFKP 439
Db 258 FNRRCHSANLNGVYSGPYTAKTDNGIVWYWTM-----HGMWYSLKSVVVKIRPDSFIP 309
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RESULT 13
O95841 PRELIMINARY; PRT; 491 AA.
AC O95841;
DT 01-MAY-1999 (TREMBLrel. 10, Created)
DT 01-MAY-1999 (TREMBLrel. 10, Last sequence update);
DT 01-OCT-2002 (TREMBLrel. 22, Last annotation update);
DE Angiopoietin Y1 (DU595C2.2) (Angiopoietin-related protein 1 precursor).
GN DU595C2.2 OR ARP1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Heart;
RX MEDLINE=99148929; PubMed=10025962;
RA Kim I., Kwak H.J., Ahn J.E., So J.N., Liu M., Koh K.N., Koh G.Y.;
RT "Molecular cloning and characterization of a novel angiopoietin family
RT protein, angiopoietin-3.";
RL FEBS Lett. 443:353-356(1999).
RN [2]
RP SEQUENCE FROM N.A.
RA Cobley V.;
RL Submitted (OCT-2000) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE=Placenta;
RA Ota T., Nishikawa T., Kawai Y., Suzuki Y., Ishii S., Saito K.,
RA Yamamoto J., Sugano S., Isogai T.;
RT "HRI human cDNA sequencing project.";
RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A.
RC TISSUE=Placenta;
RA Ito Y., Oike Y., Yasunaga K., Matsumoto S., Ota T., Nishikawa T.,
RA Kawai Y., Isogai T., Hamada K., Saito Y., Miyata K., Masuho Y.,
RA Suda T.;
RT "Molecular cloning and characterization of novel angiopoietin-related
RT protein (ARP4).";
RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
CR ENBL; AF107253; AAD19608.1; -.
DR ENBL; AB355520; CAC13169.1; -.
DR ENBL; AB056476; BAB43691.1; -.
DR HSP; P02671; IFZD.
CR Genew; HGNC:489; ANGPTL1.
DR InterPro; IPR002181; Fibrinogen_C.
DR Pfam; PF00147; fibrinogen_C; 1.
DR SMART; SM00186; FBG; 1.
DR PROSITE; PS00514; FIBRIN_AG_C_DOMAIN; 1.
KW Signal.
FT SIGNAL
FT CHAIN
SQ SEQUENCE 491 AA, 56719 MW, 3C4DB8DEF6CF7E99 CRC64;

Query Match 21.2%; Score 505; DB 4; Length 491;
Best Local Similarity 26.9%; Pred. No. 8.1e-26;
Matches 131; Conservative 81; Mismatches 137; Indels 138; Gaps 15;

QY 47 GKCEAGECPYQVSLPPLTIQIP-----KQFSRIEEVF--KEVONLKEIYNSLKKSCQ 97
Db 42 GK-EBAKKAY:FLVPEQRIITGICVNTKGQDASTIKDMITMDLENLKDVSROKREID 100
QY 98 DCKLQADDNGPGRNGLLPSTGAPGEVGNRVRELESEVNNKLSSELKNAKEIINVHGR 157
Db 101 VLQVVVDVGN-----IVNEVKLLRKESRNMNSRVQLYVQ 136
QY 158 L-----EKLNLVNMNNIENV-----DSKVNLTFVVS-----J 187
Db 137 LLEHTRKRDNSLELSQLENKILNVTTEMLKMATRYRELEVKYASLTDLVNQSVMITLL 196
QY 188 DCKCKSCPQEQIQSRP-----VQHLL----- 208
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Db 197 BEQCURTESROGTHWS2PLVQVWQHINPSOQYTPGLGGNEIGEDFGYPRDLMPFPLA 256
Qy 209 -----IYXCSDDYVAIGKRSSEYVAVTFDPKNSSEFYCDMETMG 249
Db 257 TSPTKSPFKIPVTFINEGPFKDCQAKAGSVSGIYMIKPENSGMQLWCENSLOPG 316
Qy 250 GWTVLOALDGSINFTTRMCQYKAGFGLNREFWLGNDKIHLLTKSKEMILRIDLEDFNG 309
Db 317 GWTVICAKTDSVNPFRKWNKKGFGNIDGGEYWLJLENIYLSNQNKYLIEEENSD 376
Qy 310 VELXALYQDFVANEFLKYRLHVGNNGTAGDARFNKHYHDLKFFTPDKNDRYPSG 369
Db 377 KKVVAEYSSFLPESEFYRLLEGTGYCQAGDSMMW-----HNGKQFTTLDREKXY-AG 430
Qy 370 NCGLYSSGWFACDCLSANLNGKYH-QXYRGV-RNGIFWYTWGVSEAHDPGGYKSFKE 427
Db 431 NCAHFHKGWYNACAHSNLNGWYRGHRYRSKQDGIFWAEYRG-----GSY--SLRA 492
Qy 428 AKMMIRP 434
Db 483 VQMMIKP 489
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RESULT 14

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Q9HBP3 PRELIMINARY; PRT; 244 AA.
AC Q9HBP3;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DE 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Hypothetical protein.
CS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN 1;
RP SEQUENCE FROM N.A.
RA Gu J.R., Wan D.F., Zhao X.T., Zhou X.M., Jiang H.Q., Zhang P.P.,
RA Qin W.X., Huang Y., Qiu X.K., Qian J.F., He L.P., Li H.N., Yu Y.,
RA Yu J., Han L.H.;
RT "Novel Human cDNA clones with function of inhibiting cancer cell
RT growth.";
RL Submitted (DEC-1999) to the EMBL/GenBank/DBAJ databases.
DR EMBL; AF218015; AAG17257.1; -.
DR HSBP; PC2672; 1FZD.
DR InterPro; IPR002181; Fibrinogen_C.
DR Pfam; PF00147; fibrinogen_C_1.
DR SMART; SM00186; FBG; 1.
DR PROSITE; PS00514; FIBRIN_AG_C_DOMAIN; 1.
KW Hypothetical protein.
SQ SEQUENCE 244 AA; 27825 MW; E9D0ACBF87A7139E CRC64;
```

```
Query Match 20.9%; Score 496; DB 4; Length 244;
Best Local Similarity 38.9%; Pred. No. 1.3e-25;
Matches 102; Conservative 43; Mismatches 35; Indels 22; Gaps 6;
Qy 177 VANLTFVNSLDGKCKSPSEQIQSRPVQHLIYKCDSDYVAIGKRSSEYVAVTFDPKNS 236
Db 4 VNLLTMTSINSKSDPTVAKEEQIS-----PRDCAEVFKSGHTNGYTLTFPHSTE 55
Qy 237 SFVEVCDMETGGWTVLQARLDGNTFRTRWQYKAGFGLNREFWLGNDKIHLLTKSK 296
Db 56 EIKAYCDMEAGGGWTTICREDGSDVDFORTWKEYKVGFGNPSSEYWLGNSEFVCLTNQ 115
Qy 257 EVILRIDLEDFNGVELYALDYQFYVANEFLKYRLHVGNNGTAGDARFNKHYHDLKFF 356
Db 116 RVLKIH-LKDAEGNEAYSLEYSEHLYLSSELNRYIHLKGLTGTAGKLSISQPGND---F 171
Qy 357 TTPDKNDRYSGNCGLYSSGWFADCLSANLNGKYHFKYRGVR-NGIFWTPGVSE 415
Db 172 STKGDNDKCI-C-KCSQMLTGSWGFADGSPSLNGWYYPQRNTNKENG-KWYTWK- 227
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Qy 416 AHGGYKSSFKAKMMIRPKHF 437
Db 228 ---SGY--SLKATMMIRPADF 244
RESULT 15
Q90219 PRELIMINARY; PRT; 513 AA.
AC Q90219;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Angiopoietin-1.
DE Angiopoietin-n-1.
DE ANGPT1 OR ANG1.
OS Brachydanio rerio (Zebrafish) (Danio rerio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_TaxID=7955;
RN 1;
RP SEQUENCE FROM N.A.
RA Pham V.N., Roman B.L., Weinstein B.M.;
RT "Isolation and expression analysis of three zebrafish angiopoietin
RT genes.";
RL Dev. Dyn. 221:470-474 (2001).
DR EMBL; AF379602; AAK83347.1; -.
DR ZFIN; ZDB-GENE-010819-1; angpt1.
DR InterPro; IPR002181; Fibrinogen_C.
DR Pfam; PF00147; fibrinogen_C_1.
DR SMART; SM00186; FBG; 1.
DR PROSITE; PS00514; FIBRIN_AG_C_DOMAIN; 1.
SQ SEQUENCE 513 AA; 58360 MW; C627777A39847D8B CRC64;
Query Match 20.7%; Score 491.5; DB 13; Length 513;
Best Local Similarity 26.6%; Pred. No. 6.8e-25;
Matches 142; Conservative 86; Mismatches 179; Indels 127; Gaps 16;
Qy 8 WJSSAVLATYGFVLVANNETEELKDERAKDVCPVLESRKCE---EAGECPYQVSLPPL 64
Db 2 WWCLEFLA--ALLVADVCGVEQKTDGLWSSTPKNSSSGRRYHRIHQGCSTFILPES 59
Qy 65 TIQLPKOF-----SRIEEVKE-VQNLKEIVNSLKSC 96
Db 60 DGTCTREFKSGTAYNANALQORAPQPEADLSNOKIQOLEHVNENYQWLQKINYEIKDM 119
Qy 97 QCKLQADDNGDPRNGLLLPSTGAPGEVGDN-----RVRESEV----- 137
Db 120 KTEMVQLQSSAVHNHTAAML-----EMGTSLLSQTAEQTRKLTQVETQVLNQTSRLEI 172
Qy 138 -----NKLSELKNAKEEINVLIH---GRLE-----KLNLVNMNINHYVDS 175
Db 173 OLLENSLSTNKLKLEKQIMQINEINKITHDKNGFLKEXMQELEDHRHROELESRTKESDLQA 232
Qy 176 KVANTLTFVNSLDGKCKSPSEQIQSRPVQHLI----- 209
Db 233 LVSRQSSVIRELENQLSRATNGSTALORQOQDLMSRSLLS;CAKDAATAVEPNSTKA 292
Qy 210 -----YKCDSDYVAIGKRSSEYVAVTFDPKNSSEFYCDMETGGWTVLQARLDGNTF 264
Db 293 DEERKPRDCADLYQAGFQNGVYVYTNISQETK-KVYCVNESAGSGWTVIQKREDGTVPF 351
Qy 265 TRFMQYKAGFGLNREFWLGNDKIHLLTKSKEMILRIDLEDFNGVELYALDYQFYVANE 324
Db 352 QKTMKYKYGFGFSVSGEHLNGEFVHLTNQHGRLRVLSQDWDGHOAFSQVDSFHDSE 411
Qy 325 FLKYRLHVGNNGTAGDARFNKHYHDLKFFTPDKNDRYPSGNGCYYSGGWGFAD 384
Db 412 KQKYRLFPLKTHSTAGTACQSSLAHV-CAQ---FSTKDVNDNC-TCKCALWLSGGWYDAC 466
Qy 385 LSAVLKGYHYQ-KYEGVRNGIFWTPGVSEAHDPGGYKSFKEADMMIRPKHF 437
Db 467 GPSNLGAVVYRQCHVGKFKNGIKWHYFKGPS-----YSRSTVMMIRGADP 512
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Search completed: November 5, 2003, 16:47:34
Job time : 61.0176 secs

QY 1 MFLANWYLLSSAVLATYGVFLVANNETEEIKDERAKOVCPVRLSRGCKREAGECPYQVS 60
DB 1 XRLPGWMLSSAVLAACR-AVEEHNLTGLEDAGAAACPARJEGSGRC-EGSQCPQLT 58
QY 61 LPPLTICLPKQFSRIEEVFKEVQNLKETVNSLKKSCQCKLQADCGCPGRNGLLPSTG 120
DB 59 LPTLTICLPKQFSRIEEVFKEVQNLKETVNSLKKSCQCKLQADCHRPFGNG-----GNG 114
QY 121 APGEVGNVRVRESEVKNLSSELAKNAKEEINVHGRLEKLNVMNNIENYVDSKYANL 180
DB 115 AE-TAESRVQELSQVNLKLSSELAKNAKDQIQG-QGRLETLHLVMNNIENYVKNKYANL 173
QY 181 TFVNSLDGKCKSPSQSOIQSRPVQHLYKDCSDYVAIGKSSSETYRVTPDPKNSSEV 240
DB 174 TVVNSLDGKCKSPSQSOIQSRPVQHLYKDCSDYVAIGKSSSETYRVTPDPKNSSEV 233
QY 241 YCDMETGGGTVLQARLDGSTNFTRTWQDYKAGFGNLPRFFWLGNDKIHLLTKSKVIL 300
DB 234 YCDMETGGGTVLQARLDGSTNFTREKDYKAGFGNLPRFFWLGNDKIHLLTKSKVIL 293
QY 301 RIDLEDNGVELYALYDQFYVANBEFLKYLRLHVGNNGTAGDALRPNKHVHDLKFTTPO 360
DB 294 RIDLEDNGVELYALYDQFYVANBEFLKYLRLHVGNNGTAGDALRPNKHVHDLKFTTPO 353
QY 361 KNDRYPSGNGGLYSSGWMFDCALSLANLNGKYHOKYRGVNGIPWGTAPGVSEAHFGG 420
DB 354 KNDRYPSGNGGLYSSGWMFDCALSLANLNGKYHOKYRGVNGIPWGTAPGVSEAHFGG 413
QY 421 YKSSFKKAKMMIRPKHKFP 439
DB 414 YKSSFKKAKMMIRPKHKFP 432

RESULT 3

AAR65759

ID AAR65759 standard; protein; 314 AA.

XX

AC AAR65759;

XX 25-MAR-2003 (updated)

DT 17-MAY-1995 (first entry)

XX

DE Rat hepatic parenchymal cell growth factor.

XX Hepatic parenchymal cell growth factor; HPGF; liver diseases;

XX liver cancer; cirrhosis.

XX

CS Rattus rattus.

XX

FH Key Location/Qualifiers

FT Peptide

FT /label= sig_peptide

XX

XX W03421678-A1.

XX

XX 29-SEP-1994.

XX

PF 22-MAR-1994; 94WO-JP00455.

XX

PR 23-MAR-1993; 93JP-0063905.

XX

PA (TAIS) TAISHO PHARM CO LTD.

XX

PI Hanada K, Hara H, Matsuki Y, Shindo S, Yoshimura H;

XX

XX WPI; 1994-316940/39.

XX

DR N-PSDB; AAR65759.

XX

PT Hepatic parenchymal cell growth promoter peptide - is isolated from human or animal liver cell; or produced by recombinant techniques and used for therapy of liver diseases

XX

XX Claim 3; Page 34; 47pp; Japanese.

XX AAQ77818 encodes AAR65759 rat hepatic parenchymal cell growth factor (HPGF). The protein or the N-terminal peptide (AAR65759) may be used in the diagnosis and treatment of liver diseases, such as liver cancer and cirrhosis.
CC
CC (Updated on 25-MAR-2003 to correct PN field.)
XX

SQ Sequence 314 AA;

Query Match 22.0%; Score 524; DB 15; Length 314;
Best Local Similarity 37.6%; Pred. No. 1.7e-38;
Matches 124; Conservative 46; Mismatches 104; Indels 56; Gaps 13;

QY 125 VGD-NAVRE---JSEVVKLSSELAKNAKEEINVHGRLEKLNVMNNIENYVDSKYANL 179
DB 23 LGDENCLOQVLRACVQLQTRVQKQVQVIAQLLHEK--EVQFLDRGQEDSFID----- 75

QY 180 LTFVNSLDGKCKSPSQSOIQSRPVQHLYKDCSDYVAIGKSSSETYRVTPDPKNSSEV 239
DB 76 -----LGKK-----RH--YADCSEIYNDGFKHSGFYKIKPQSLAEFS 111

QY 240 YCDMETGGGTVLQARLDGSTNFTRTWQDYKAGFGNLPRFFWLGNDKIHLLTKSKVIL 296
DB 112 VYCDMSD-CGGWTVLQRRSDGSENFNRGNDYENGFGNFVQSGNGEVLGNKNILNLTWQ 170

QY 297 ENILRIDLEDNGVELYALYDQFYVANBEFLKYLRLHVGNNGTAGDALRPNKHVHDLKFTTPO 360
DB 171 DYLKIDLTDFEKNRFAQYERKPKVGDKSPFELNIGESGTAGDSLSGT.FHPEVOMWAS 230

QY 351 HOLKFTTTPDKNDRYPSGNGGLYSSGWMFDCALSLANLNGKYHOKYRGVNGIPWGTAPGVSEAHFGG 420
DB 231 RQTKFESTERNDNY-NGNCABEESGWMFNRCHSANLNGYCYCPYRAETDNGVVWYT 289

QY 410 WPGVSEAHFGGYKSSFKKAKMMIRPKHKFP 439

DB 290 W-----RGWYSLKSVVMKIRPSDFIP 311

RESULT 4

AAR61411

ID AAR61411 standard; Protein; 496 AA.

XX

AC AAR61411;

XX

DT 11-FEB-1997 (first entry)

XX

DE Human TIE-2 ligand 2.

XX

XX TIE-2 ligand 2; tyrosine kinase with Ig and EGF homology domain;

XX receptor; antagonist; neovascularisation; wound healing; ischaemia;

XX leukaemia; thrombocytopaenia; anaemia; angiogenesis; tumour;

XX atherosclerosis; inflammation; diagnosis; therapy.

XX

OS Homo sapiens.

XX

XX W09631598-A1.

XX

XX 10-OCT-1996.

XX

XX 05-APR-1996; 96WO-US04906.

XX

XX 06-OCT-1995; 95WO-US12935.

XX

XX 06-APR-1995; 95US-0418595.

XX

XX (REG-) REGENERON PHARM INC.

XX

XX A. Dr. J. H. Bruto J. Davis S. Goldfarb M. Jones P.

XX Waissonpierre PC, Radziejewski C, Yancopoulos GD;

XX WPI; 1995-465021/46.

XX

XX R-PSDB; AA-44321.

XX

XX TIE-2 agonists and antagonists and related DNA - useful for

PT promoting or blocking neovascularisation, etc

XX Claim 15; Fig 6; 113pp; English.

XX Human TIE-2 (tyrosine kinase with Ig and EGF homology domains)
 CC ligand 2 (AA031411) is a ligand that binds the TIE-2 receptor. Its
 CC amino acid sequence was deduced from a cDNA clone (AA044321) derived
 CC from human foetal lung cells. TIE-2 ligand 2 is a receptor
 CC antagonist useful for blocking blood vessel growth, for tumour
 CC therapy and for treating a proliferative disorder of a blood-
 CC forming organ. It can be obt'd. from natural sources or expressed
 CC in transformed host cells.

XX Sequence 496 AA;

Query Match 22.0%; Score 522; DB 17; Length 496;

Best Local Similarity 27.9%; Pred. No. 5.2e-38;

Matches 138; Conservative 74; Mismatches 159; Indels 124; Gaps 15;

OY 43 LESRGKCE---EAGECPYQVSLPPL-----TIQ--LPKQFSRIEVEFKEVQN 84

DB 26 MDSIGKKYQVQHGSCSYTFLLPEMNCNCRSSSPYVNAVQDAPLEYDSDVQR-QVLEN 85

OY 85 LKE-----IVNSLKKSCQCKLQADNGDPGRNGLLPSTGAPGEVDN---- 128

DB 86 IMENNTQWLKLENYIQDNMKEMWZIQQNAVQ-----CTAVMIEGTNLLNQ 134

OY 129 -----RVRELESEV-----NKLSSSELKNAKEEINVLHGR---LEKL 161

DB 135 TAEQTRKLTDEVAQVLNQTTRELQLEHSLSTNLEKQILDTSEINKLQDKNSFJEKK 194

OY 162 NLV-----N'NLENVYDVKVANLTF-----V 183

DB 195 VLAMEDKHIIQLOSKEEKQOQVLSVKQNSIELEKXIVTATVNSVLQKQCHLMET 254

OY 184 VNSLDGKCKSCPSQEQIQSRPVQHLLYKDCSDYYAIGKRSSSETRYVTPDPQNSFEVCD 243

DB 255 VNNLLTVMKSTNSAKDPTVAKEEQISFRDCAEVFKSGHTTNGIYTLTPNSTEEIKAYCD 314

OY 244 METVGGGWTVLQARLDGSGNFTTWODYKAGFONLRREFWLGNDKIHLLTKSKEXILRID 303

DB 315 MEAGGGGWTIIORREDGSDVDFORTWKEYKVGFGNPSGEYWLGNFVSLTNQRYVLKIH 374

OY 304 LEDFNGVELYALYDQFVANEFLKYLHLVGNVNYGTAGDALRPNKHYNHDLKFFTTDPKON 363

DB 375 JKDWEENEAYSIEHYISSEELNRIHLKGLTGTAGKSSISQFQND-----FTYDQGN 430

OY 364 DRYPSGNCGLYYSSGWWFDACLSANLNGKYYFKYRGYR-NGIFAGTWFGVSEARPGGYK 422

DB 431 DKCIC-KCSQXJTGWWFDPACGPNLNGMYYPQRCNTKKNFCIKYYNKG-----SGY- 482

OY 423 SSFPEAKVMIRPEKH 437

DB 483 -SLKATTMIRPADF 496

XX AAR94605;

XX 28-OCT-1996 (first entry)

XX Human TIE-2 ligand 2 derived from pBluescript KS clone.

XX Angiogenesis; neovascularisation; tumour development; wound healing;

XX TIE; tyrosine kinase with Ig and EGF homology domains; vector;

XX recombinant; clone; diagnosis; ischaemia; thromboembolytic disease;

XX atherosclerosis; inflammation; diabetes; ligand bodies; delivery;

XX targeting.

XX Homo sapiens.

OS

XX WC3611269-A2.
 XX 18-APR-1996.
 XX 06-OCT-1995; 95KO-JS12935.
 XX 06-APR-1995; 95US-C418595.
 XX 07-OCT-1994; 94US-0319912.
 XX 27-OCT-1994; 94US-0330261.
 XX 02-DEC-1994; 94US-0348492.
 XX 09-DEC-1994; 94US-0353503.
 XX 17-JAN-1995; 95US-0373575.
 XX (REGG); REGENERON PHARM INC.
 XX Aldrich TH, Bruno J, Davis S, Geldfarb M, Jones PF;
 XX Maisonnier PC, Radziejewski C, Yancopoulos GD;
 XX N-PSDB; AAT14650.
 XX WP; 1996-209850/21.
 XX Nucleic acid encoding TIE-2 ligand and related vectors - useful in
 XX diagnosis and treatment of neovascularisation, tumours, etc., cr to
 XX promote wound healing, etc.
 XX Claim 2; Fig 6; 84pp; English.
 XX AAR94605 is a human TIE-2 (hTIE-2) ligand 2 derived from a pBluescript
 XX KS clone. hTIE-2 ligand DNAs of the invention are recombinant versions
 XX of the native ligand coding sequences and may be used to produce the
 XX ligands at a high yield. Antibodies and receptor bodies that bind to
 XX TIE-2 ligands may be used to inhibit angiogenesis and neovascularisation
 XX (e.g. associated with tumour development) and the TIE-2 ligands
 XX themselves are useful to promote neovascularisation and wound healing
 XX e.g. for treatment of ischaemia. TIE-2 ligands are also useful to
 XX treat thromboembolytic disease, atherosclerosis, inflammation and
 XX diabetes. Ligand bodies contg. TIE-2 ligands may also be useful for
 XX the delivery and targeting of growth factors, toxins etc. to sites
 XX where their presence is advantageous.

Sequence 496 AA;

Query Match 22.0%; Score 522; DB 17; Length 496;

Best Local Similarity 27.9%; Pred. No. 5.2e-38;

Matches 138; Conservative 74; Mismatches 159; Indels 124; Gaps 15;

OY 43 LESRGKCE---EAGECPYQVSLPPL-----TIQ--LPKQFSRIEVEFKEVQN 84

DB 26 XDSIGKKYQVQHGSCSYTFLLPEMNCNCRSSSPYVNAVQDAPLEYDSDVQLQVLEN 85

OY 85 LKE-----IVNSLKKSCQCKLQADNGDPGRNGLLPSTGAPGEVDN---- 128

DB 86 IMENNTQWLKLENYIQDNMKEMWZIQQNAVQ-----CTAVMIEGTNLLNQ 134

OY 129 -----RVRELESEV-----NKLSSSELKNAKEEINVLHGR---LEKL 161

DB 135 TAEQTRKLTDEVAQVLNQTTRELQLEHSLSTNLEKQILDTSEINKLQDKNSFJEKK 194

OY 162 NLV-----N'NLENVYDVKVANLTF-----V 183

DB 195 VLAMEDKHIIQLOSKEEKQOQVLSVKQNSIELEKXIVTATVNSVLQKQCHLMET 254

OY 184 VNSLDGKCKSCPSQEQIQSRPVQHLLYKDCSDYYAIGKRSSSETRYVTPDPQNSFEVCD 243

DB 255 VNNLLTVMKSTNSAKDPTVAKEEQISFRDCAEVFKSGHTTNGIYTLTPNSTEEIKAYCD 314

OY 244 METVGGGWTVLQARLDGSGNFTTWODYKAGFONLRREFWLGNDKIHLLTKSKEXILRID 303

DB 315 MEAGGGGWTIIORREDGSDVDFORTWKEYKVGFGNPSGEYWLGNFVSLTNQRYVLKIH 374

OY 304 LEDFNGVELYALYDQFVANEFLKYLHLVGNVNYGTAGDALRPNKHYNHDLKFFTTDPKON 363

DB 375 JKDWEENEAYSIEHYISSEELNRIHLKGLTGTAGKSSISQFQND-----FTYDQGN 430

OY 364 DRYPSGNCGLYYSSGWWFDACLSANLNGKYYFKYRGYR-NGIFAGTWFGVSEARPGGYK 422

DB 431 DKCIC-KCSQXJTGWWFDPACGPNLNGMYYPQRCNTKKNFCIKYYNKG-----SGY- 482

OY 423 SSFPEAKVMIRPEKH 437

DB 483 -SLKATTMIRPADF 496


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Db 375 LKDWEGNEAYSLYERFYLSSSEELNRYHLKGTGTAGKISS:SQPGND-----FSTKGDGN 430
QY 364 DRYPSGNCGLYSSGWDFDACLUSANLNGYHYHCKYRGVR-NGIFWGTWPGVSEAHFGGYK 422
Db 431 DKCIC-KCSQMLTGGWDFDAGCSNLNGMYYPQONTNKFNGIKWYWKG-----SGY- 482
QY 423 SSFKEAKMIRPKHF 437
Db 483 -SLKATTMIRPADP 496

RESULT 6
ID AAW47532
XX AAW47532 standard; Protein; 496 AA.
AC AAW47532;
XX
DI 09-SEP-1998 (first entry);
DE Human TIE-2 ligand 2 from clone pBluescript KS.
KW Chimeric TIE ligand 2NICF; TIE-2 ligand; neovascularisation;
KW tumour; human.
OS Homo sapiens.
EN WO9805779-A1.
XX
FD 12-FEB-1998.
XX
PF 01-AUG-1997; 97MO-US13557.
XX
PR 25-OCT-1996; 96JUS-0740223.
PR 02-AUG-1996; 96US-0222999.
XX
PA (REG-) REGENERON PHARM INC.
PI Davis S. Yancopoulos GD;
DR WPI; 1996-145615/13.
DR N-PSDB; AAV18619.
XX
PT Modified human TIE-2 receptor ligand(s) - useful for promoting wound
PT healing
XX
PS Example 8; Fig 6; 202pp; English.
XX
CC This is the amino acid sequence of the human TIE-2 ligand 2,
CC used in the method of the invention, involving the production
CC of TIE-2 ligands which promote healing. The nucleic acids, vectors
CC and host cells used in the method of the invention are useful for
CC the recombinant production of the ligands. The ligands, etc. are
CC useful for blocking blood vessel growth, promoting neovascularisation,
CC promoting the growth or differentiation of a cell expressing the TIE
CC receptor, blocking the growth or differentiation of a cell expressing
CC the TIE receptor and for attenuating or preventing tumour growth in
CC a human.
XX
SQ Sequence 496 AA;

Query Match 22.0%; Score 522; DB 19; Length 496;
Best Local Similarity 27.9%; Pred. No. 5.2e-38;
Matches 138; Conservative 74; Mismatches 159; Indels 124; Gaps 15;

QY 43 LSESGKCE---EAGECPYQVSLPPL-----TIQ--LPQPSRIEEVKEVON 84
Db 26 MDSIGKKQVQHGSCSY7FLLPENDENCRSSSPYVSNVQRPAPJEDYDSDYQRIQVLEN 95
QY 85 LK2-----IWSLKKSCQCKLQADNDGPPGNGLLPSTGAPGVDGN--- 128
Db 86 IMENN-QWLMKLENYIQDKKKSMVEIQNAVNQ-----QTAVNIGIYNLNLQ 134
QY 129 -----RVRELESEV-----NKLSSSEJKNAKEEINYLHGR---LEKL 161

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Db 135 TABQTRKLTDEACVLNQTRLEQLLEHSLSTNKLKQLIOOTSEINKLQDKNSFLEKK 194
QY 162 NLV-----NMNINENYVDSKVANLT7F-----V 183
Db 195 VLAMEDKHIIQLQSIKEEKDQLVLVSKNSIIEELEKKIVTATVNNSVLQKQCHDLMET 254
QY 184 VNSLDGKCKSPQEQIOQRPVQHLLYKDCSDYAYAGKSSSETYRVTPDKNSSFEVYCD 243
Db 255 VNNLTVMSTNSAKDPTVAXEQISFRDCAEVFKSGHTINGIYTLTFPNSTEEIKAYCD 314
QY 244 METMGSGMTVLQARLQSGSTNFTRTWQDYKAGFCNLRREFWLGNDKHLTLTKSKEMILRID 303
Db 315 MEAGGGGWTIIQRDEGSDVDFTWKEKYKVGFCNPSGEYWLGNFVSQLTNQGRYVLKCH 374
QY 304 LEDFNGVELYALYDQFYVANEFLKYLHLVGNNGTAGDALRPNKHNHDLKFTTTPDKDN 363
Db 375 LKDWEGNEAYSLYERFYLSSSEELNRYHLKGLTGTAGK-SSISQPGND----FSTKGDGN 430
QY 364 DRYPSGNCGLYSSGWDFDACLUSANLNGYHYHCKYRGVR-NGIFWGTWPGVSEAHFGGYK 422
Db 431 DKCIC-KCSQMLTGGWDFDAGCSNLNGMYYPQONTNKFNGIKWYWKG-----SGY- 482
QY 423 SSFKEAKMIRPKHF 437
Db 483 -SLKATTMIRPADP 496

RESULT 7
ID AAB28392
XX AAB28392 standard; Protein; 496 AA.
AC AAB28392;
XX
DI 19-FEB-2001 (first entry);
DE Human angiopoietin-2.
XX
KW Human; angiopoietin-2; cytostatic; antiproliferative;
KW vascular endothelial growth factor; VEGF; antibody; VEGF2 receptor;
KW blood vessel regression; cancer; vascularised solid tumour.
XX
OS Homo sapiens.
EN WO2000064946-A2.
XX
PD 02-NOV-2000.
XX
PF 28-APR-2000; 2000WO-US11367.
XX
PR 28-APR-1999; 99US-0131432.
XX
PA (TEXA ) UNIV TEXAS SYSTEM.
PI Thorpe PE, Brekken RA;
DR WPI; 2000-687317/67.
DR N-PSDB; AAC67774.
XX
XX Immunogenic composition for the treatment and diagnosis of cancer
XX comprises an anti-VEGF (vascular endothelial growth factor) antibody
XX binding the same epitope as the monoclonal antibody ATCC PTA 1595 -
XX
XX Disclosure; Page 283-285; 298pp; English.
XX
XX The present invention relates to anti-Vascular Endothelial Growth Factor
XX (VEGF) antibodies that bind to the same epitope as the monoclonal
XX antibody ATCC PTA 1595 and which significantly inhibit VEGF binding to
XX the VEGF receptor VEGFR2, without inhibiting VEGF binding to the VEGF
XX receptor VEGFR1. The present sequence is human angiopoietin-2.
XX Angiopoietin-2 may be operatively attached to the anti-VEGF antibodies of
XX the present invention. Angiopoietin-2 acts to disturb capillary structure
XX and is thought to lead to vessel regression. The anti-VEGF antibodies of

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CC the present invention are useful for the treatment and diagnosis of
CC cancer, especially vascularised solid tumours.

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AX	Sequence	496 AA;
SC		

Query Match 22.08; Score 522; DB 21; Length 496;

Best Local Similarity 27.9%; Pred. No. 5.2e-38;

Matches 138; Conservative 74; Mismatches 159; Index's 124; Gaps 15;

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CY      43 LESRGKE--ENGECYVVSLLPL-----T-Q-LEKQFSRIEVEFEVCVN 94
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26 NDSIGKKQYQVHGSCSYFLLPENDNCRSSSSPVGSHAVQRDAFLFYDDSVORLQVLEN 35

2b 86 IMENNTQWLMKJENYIQDNKKEMVEIQQNAVGN-----QTAVMIEIGTNLLNQ 134

Qy	129	-----RVRELESEV-----NKJSEZJNAKEEINVJHGR-----LEK. 161
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DB	135	TAEQTRKLTQDVEAQVLNQ---	RLEQLLEHS-STNK-EKQILDQTS-	NK-QDKGSLLEK	191
CW	162	NLV-----	NMRN-ENYVDSKVANIET-	-V	183

162 NLV-----NMNK--ENYVDSKVAALTF--V 18
CY
195 VLAVEDKHIIQLQS:KEEDQQLQVLVSKNS:IEELEKXIVTATWNSVLQKQCOHLMNET 254
Cb

```
QY      184  VNSLDGKSCKCPQEQIQSRFVQHLLIYKDCSDYYAIGKRSSEYRVTPDPKNSSFVYCD 243
```

db 255 VNLLTMS*SNSAKPTVAKEEQISFRDCAEVFKSGHTTNGIXTL:FPNST:EE:KAYCD 314

QY	244	245	246	247	248	249	250	251	252	253	254	255	256	257	258	259	260	261	262	263	264	265	266	267	268	269	270	271	272	273	274	275	276	277	278	279	280	281	282	283	284	285	286	287	288	289	290	291	292	293	294	295	296	297	298	299	300	301	302	303	304	305	306	307	308	309	310	311	312	313	314	315	316	317	318	319	320	321	322	323	324	325	326	327	328	329	330	331	332	333	334	335	336	337	338	339	340	341	342	343	344	345	346	347	348	349	350	351	352	353	354	355	356	357	358	359	360	361	362	363	364	365	366	367	368	369	370	371	372	373	374	375	376	377	378	379	380	381	382	383	384	385	386	387	388	389	390	391	392	393	394	395	396	397	398	399	400	401	402	403	404	405	406	407	408	409	410	411	412	413	414	415	416	417	418	419	420	421	422	423	424	425	426	427	428	429	430	431	432	433	434	435	436	437	438	439	440	441	442	443	444	445	446	447	448	449	450	451	452	453	454	455	456	457	458	459	460	461	462	463	464	465	466	467	468	469	470	471	472	473	474	475	476	477	478	479	480	481	482	483	484	485	486	487	488	489	490	491	492	493	494	495	496	497	498	499	500	501	502	503	504	505	506	507	508	509	510	511	512	513	514	515	516	517	518	519	520	521	522	523	524	525	526	527	528	529	530	531	532	533	534	535	536	537	538	539	540	541	542	543	544	545	546	547	548	549	550	551	552	553	554	555	556	557	558	559	560	561	562	563	564	565	566	567	568	569	570	571	572	573	574	575	576	577	578	579	580	581	582	583	584	585	586	587	588	589	590	591	592	593	594	595	596	597	598	599	600	601	602	603	604	605	606	607	608	609	610	611	612	613	614	615	616	617	618	619	620	621	622	623	624	625	626	627	628	629	630	631	632	633	634	635	636	637	638	639	640	641	642	643	644	645	646	647	648	649	650	651	652	653	654	655	656	657	658	659	660	661	662	663	664	665	666	667	668	669	670	671	672	673	674	675	676	677	678	679	680	681	682	683	684	685	686	687	688	689	690	691	692	693	694	695	696	
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315	MEAGGSGWTIIQRREDGSDVFQRTWKKEYKVGFGNPSGEYWLGNBFPVSQLTNQQRYYVLKIH	374
Db		
304	IEDENGVELYALYDFOFYVANEELKYRIHVGNVNGTAGDAIRENKHYVNHDIKFEFTTDPKDN	363
OV		

375 LKDWEGEAYSLEYHFYLSSEELNRIHLKGLGTAGKISSSQPGND----FSTKGGDN 430

QY 364 DRYPSGNCGLYYSGGWFFDACL SANLNGKYHQYRGVR-NGIFGFWPGVSEAHPGYK 422

3D 431 DKCIC-KLSQMETGGWNF-DACGPNJNGMYIFQKQNTAKKNGIRKIYWRG-----SGI-485
QY 423 SSFKEAKMMIRPKHF 437

47 423 -REAGHARTEN 437
| | | | |
25 433 -SLKATMMIRPADF 496

RESULT 8

AAV78903
:C AAV78903 standard; Protein; 496 AA.
v

AC
AAV78903;

XX

XX

DE Human angiotensinogen-2 amino acid sequence.

XX

:KW Angiopoietin-2; Ang-2; vascular endothelial

KW: vascularisation; angiogenesis; blood vessels

benign; binding liquid; cancer; aminophos

[illegible]

Homosapiens.

XX
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NO2C0002587-A1

XX
WJZC0002587-AT.

20--JAN-2000

20-JAN-2000.
XX

XX
XX
8395-3.1-UM000

12-JUL-1999; 6667-707-21
6666-6667-6668.

[illegible]

13-JUL-1998; 98JS-0092589.

PR 02-DEC-1998; 98JS-0110600.

ID AAY78906 standard; Protein; 496 AA.
 XX AC AAY78906;
 XX DT 19-MAY-2000 (first entry)
 XX DE Human angiotensin-2 (Ang-2); amino acid sequence.
 XX KW Human; angiotensin-2; Ang-2; aminophospholipid; vascularised tumour;
 KW unjugated anti-aminophospholipid antibody; tumour blood vessel marker;
 KW cancer; treatment; angiogenesis.
 XX OS Homo sapiens.
 XX PN WO200002584-A2.
 XX PD 20-JAN-2000.
 XX PF 12-JUL-1999; 99WC-US15600.
 XX PR 13-JUL-1998; 98US-0032672.
 XX PR 02-DEC-1999; 98US-C110608.
 XX PA (TEXA) UNIV TEXAS SYSTEM.
 PI Thorpe PE, Ran S;
 XX WP1; 2000-182175/16.
 XX N-PSDB; AAZ92225.
 XX New composition for killing tumour vascular endothelial cells for
 PT treating solid tumours, comprises unconjugated anti-aminophospholipid
 PT antibody -
 XX Disclosure; Page 223-224; 226pp; English.
 XX This sequence represents the human angiotensin-2 (Ang-2) amino acid
 CC sequence. Ang-2 is a naturally occurring angiogenesis antagonist when
 CC vascular endothelial growth factor (VEGF) levels are low, and generally
 CC counteracts the blood vessel maturation and stability mediated by Ang-1.
 CC Ang-1 is a naturally occurring angiogenesis agonist, and is a maturation
 CC or stabilisation factor, converting immature vessels to mature vessels.
 CC Both Ang-1 and Ang-2 are useful in a therapeutic approach to the
 CC treatment of vascularised tumours. The invention relates to a composition
 CC comprising an anti-aminophospholipid antibody, or its antigen binding
 CC region. The composition is used to kill tumour vasculature endothelial
 CC cells. Aminophospholipids are stable and specific markers accessible on
 CC the luminal surface of tumour blood vessels. Ang-1 or Ang-2 may be used
 CC in the composition of the invention. The composition is used to treat
 CC malignant or benign vascularised tumours in animals, especially large
 CC tumours.
 XX SQ Sequence 496 AA;
 Query Match 22.0%; Score 522; DB 21; Length 496;
 Best Local Similarity 27.9%; Pred No. 5.2e-38;
 Matches 139; Conservative 74; Mismatches 159; Indels 124; Gaps 15;
 QY 43 LESRKCCE---PAGECPYQVSAPPL-----TIQ--LPKQPSRIEVEFKVQN 84
 DB 26 MDSIGKKQYQVQHGGSCSYTFJLPFMDNCRSSSPYVNAVCQDAFLVDLSVQRLQVLEN 95
 QY 85 LXE-----IVNSLKSCQCEKQACDNDGFGNGLLSTGAPGVEGDN----- 128
 DB 86 IMENNTQWLKMLGNYIQCKYKKEVMEIQCAVQN-----QTAVNIEIGTNLQ 134
 QY 129 -----RVLESEV-----NKLSSSELKQAKSEINVLHGR---LEKL 161
 EB 135 TAEQTRKTDVDAQVLNQTRLEQLLESLSTNKLKXCIJGCTSEINKLQDKNSFLKK 194
 QY 162 NLV-----NMNNTIYVDSKVANLTF-----V 183
 DB 195 VLAMEDKHIIQLOSKEEKDQLQVLVSKNSIIELEKKIVATVNNSVLQNCQCHLDET 254

QY 184 VNSLDGKCKSPQEQIQSRPVQHLLYKDCSDYYAIGKSSSETYRTVPDPKNSSEFVYCD 243
 DB 255 VNNLLTWMSTNSAKDPTVAKEEQISFRDCAEVFKSGHTINGIYTLTFPNSTEIKAYCD 314
 QY 244 XETMGGGWTVLQARLDGSTNFTRTWDYXAGFGNLRREFWLGNDKIHLLTKSKEMIRID 303
 DB 315 XEAGGGGWIIQREDGSDVDFQRTNKEYKVGFGNPSGEYWLGNFVSQLTNQORYVLKIH 374
 QY 304 LEDPFGVELYALYDQFYVANEFLKYRLHGVNGYNTAGDALRFNKNYHDLKFTTPEKDN 363
 DB 375 LKDWEGNEAYSLYEHFVLSSEENYRIHLKGLTGTTAGKISSISQPGND----FSTKDGDN 430
 QY 364 DRYPSGNGCLYSSGWNEDACLSANLNGKYYHOKYRGVR-NGIFMGTWPGVSAHFGYK 422
 DB 431 DKIC-KCSQMLTGGWDFDAGPSNLNGMYYPQRTNKNFGIKRYYWKG-----SGY- 482
 QY 423 SSFKEAKNMIRPKHF 437
 DB 483 -SLKATNMIRPADF 496
 RESULT 10
 AAU77944
 IC AAU77944 standard; Protein; 496 AA.
 XX AC AAU77944;
 XX DT 02-JUL-2002 (first entry)
 XX AMiRo acid sequence for human angiotensin-2.
 XX Human; immunoconjugate; anti-vascular endothelial growth factor antibody;
 KW anti-VEGF antibody; monoclonal antibody 2C3 ATCC PTA 1595; VEGF receptor;
 KW VEGFR2; KDR/Flk-1; VEGFR1; Flt-1; angiogenesis; macular degeneration;
 KW ocular neovascular disease; cancer; vascularised solid tumour; AIDS;
 KW metastatic tumour; endothelial cell proliferation; inflammatory disorder;
 KW atherosclerosis; diabetic retinopathy; corneal graft rejection;
 KW acquired immune deficiency syndrome; infection; restenosis; fungal ulcer;
 KW sickle cell anaemia; endometriosis; angiotensin-2.
 OS Homo sapiens.
 XX AU200179401-A.
 XX C6-DEC-2001.
 XX 12-OCT-2001; 2001AU-0079401.
 XX 28-APR-2000; 2000AU-0048049.
 XX 12-OCT-2001; 2001AU-0079401.
 XX (TEXA) UNIV TEXAS SYSTEM.
 XX Thorpe PE, Brekken RA;
 XX WPI; 2002-281368/33.
 XX N-PSDB; ABK47716.
 XX Immunconjugate compositions for treating cancer by inhibiting
 PT angiogenesis and for delivering a diagnostic agent to tumour, comprises
 PT anti-vascular endothelial growth factor antibody attached to a
 PT biological agent -
 XX Disclosure; Page 4-6 (sequence listing); 300pp; English.
 XX The present invention relates to antibody-based compositions comprising
 CC an immunoconjugate such as anti-vascular endothelial growth factor
 CC (VEGF) antibody (Ab) (or its antigen-binding fragment), attached to a
 CC biological agent, where the Ab binds to the same epitope as the
 CC monoclonal antibody (MAb) 2C3 ATCC PTA 1595, and significantly inhibits
 CC VEGF binding to the VEGF receptor VEGFR2 (KDR/Flk-1) without inhibiting
 CC VEGF binding to the VEGF receptor VEGFR1 (Flt-1). The compositions

CC of the invention are useful in therapy, and diagnosis, for inhibiting
 CC angiogenesis in an animal having ocular neovascular disease or macular
 CC degeneration, and for delivering a biological agent to a vascularised
 CC tumour. The compositions can also be used for treating cancer and
 CC subjects at risk of developing a vascularised solid tumour, a metastatic
 CC tumour or metastases from a primary tumour. The composition is useful
 CC for specifically inhibiting VEGF-induced endothelial cell proliferation,
 CC without significantly inhibiting VEGF-induced macrophage, osteoclast or
 CC chondroclast function. The compositions can be used for treating various
 CC diseases such as inflammatory disorders, atherosclerosis, diabetic
 CC retinopathy, restenosis, acquired immune deficiency syndrome (AIDS),
 CC blood borne tumours, corneal graft rejection, Crohn's disease, fungal
 CC ulcers, infections, sickle cell anaemia, and endometriosis. The present
 CC sequence represents human angiopoietin-2. Angiopoietin-2 may be attached
 CC or functionally associated with anti-VEGF antibodies.

XX
 SQ Sequence 496 AA;

Query Match 22.0%; Score 522; DB 23; Length 496;
 Best Local Similarity 27.9%; Pred. No. 5.2e-38;
 Matches 138; Conservative 74; Mismatches 159; Indels 124; Gaps 15;

QY 43 LESRGKCE---EAGECPYQVSLPPL-----TIQ--LPKQFSRIEEVFKEVQN 84
 DB 26 MDSIGKKQYQVHGSCSYTFLLPEMNCSSSSSPYVSNVAVQDAPLEYDSDVQRLOVLEN 85
 QY 85 LKE-----IVNSLKSCQCKLOADNCGPGRNGLLPSTGAPGEVDN---- 128
 DB 86 IMENNTQWLKLENYIQDNKKEMVEIQQNAVQN-----QTAVMIEGTNLNC 134
 QY 129 -----RVRELESEV-----NKLSELKNAAKEEINVJHGR---LEKL 161
 DB 135 TAQTRKLTDEVAQVLNQTTRLEQLLEHSLSTNKLEKQLDQTSINKLQDKNSFLEKK 194
 QY 162 NLV-----NMNIENYVDSKVANLTF-----V 183
 DB 195 VLAMEDKHIIQLOSIKEEKQQLVLSKQNSIIEELEKXIVTATVNSVLQKQCHLMET 254
 QY 184 VNSLDGKSKCPSQEQICSRPVQHLLIYKDCSDYYAIGKRSSEYRYVTPDPKSSFEVYCD 243
 DB 255 VNNLLTMMSTNSAKDPTVAKEQISFRDCAEVFKSGHTNGTYTJTFNSEEIKAYCD 314
 QY 244 VETMGGGWTVLQARLDGSGTNFTRTWQDYKAGFGLNRREFWLNCKIHLTKSKEMILRID 303
 DB 315 NEAGGGNTIIQREDGSDVFCQWKEYKVGPNPSEYWLGNFVSLTNQQRVYVXKH 374
 QY 304 LEQFNGVELYALDQFYVAKEFLKYRHJGVNGYNGTAGDALRPNKHVYHDLKFTTPDKEN 363
 DB 375 LKQWEGNEAVSLVERFVLSSEELNYRIHLKGLTGTAGKSSISQPGNQ----PSTKQGN 430
 QY 364 DRYPAGNCGLYYSSGWFDACLSANLNGKYHHQYRGVR-NGIFKGTWPGVSEAHPGCYK 422
 DB 431 DKCIC-KCSQMLTGGWFFDACGSPNLNGWYYPQONTNFKNGIKWYWKG-----SGV- 482
 QY 423 SSFKEAKMIRPKHF 437
 DB 483 -SLKATMMIRPADF 496

RESULT 11

ABU07855

ID ABU07855 standard; Protein: 496 AA.

XX AC ABU07855;

XX XX

DT 10-MAY-2003 (first entry)

XX DE Human angiopoietin 2 (Ang-2).

XX XX

KW Cytostatic; vasodilator; antiinflammatory; cardiant; gene therapy;
 KW ligand;receptor binding modulator; ephrin ligand; angiogenesis;
 KW lymphangiogenesis; aberrant Ephrin-Tie biology; cell growth disorder;
 KW cell migration disorder; cell proliferation disorder;

KW neovascularisation; ischaemia; infarction; tissue graft; transplant;
 KW tie receptor tyrosine kinase; angiopoietin 2; ang-2; human;
 XX Tie-2 receptor tyrosine kinase ligand.

OS Homo sapiens.

XX WO2003004529-A2.

XX 16-JAN-2003.

XX 02-JUL-2002; 2002WO-IB02524.

XX 02-JUL-2001; 2001US-302963P.

XX (LICN) LICENTIA LTD.

XX Alitalo K, Kubo H;

XX WPI; 2003-210341/20.

XX N-PSDB; ABX12556.

PT Identifying modulators of binding between a Tie receptor tyrosine

PT kinase and an Ephrin ligand, useful for promoting neovascularization,

PT comprises contacting a Tie receptor with an Ephrin in the presence of a

PT putative modulator

XX Disclosure; Page 186-188; 199pp; English.

XX The invention describes a method of identifying a modulator of binding
 CC between a Tie receptor tyrosine kinase and an Ephrin ligand. The method
 CC comprises contacting a Tie receptor composition with an Ephrin
 CC composition in the presence and in the absence of a putative modulator
 CC compound, and detecting the binding between the Tie receptor and the Ephrin
 CC in the presence and in the absence of the putative modulator. The method
 CC is useful for identifying a modulator of binding between a Tie receptor
 CC tyrosine kinase and an Ephrin ligand. Modulators identified from the
 CC method are useful in modulating angiogenic processes, including
 CC lymphangiogenesis, for treating diseases associated with aberrant
 CC Ephrin-Tie biology, aberrant growth, migration or proliferation of cells
 CC that express a Tie receptor, or for promoting growth of vessel or
 CC neovascularisation (e.g. ischaemic tissue, an infarction, a new or
 CC chronic compound, or a tissue graft or transplant). This is the amino
 CC acid sequence of human angiopoietin 2 (ang-2), a Tie-2 tyrosine receptor
 CC kinase ligand.

XX Sequence 496 AA;

Query Match 22.0%; Score 522; DB 24; Length 496;

Best Local Similarity 27.9%; Pred. No. 5.2e-38;

Matches 138; Conservative 74; Mismatches 159; Indels 124; Gaps 15;

QY 43 LESRGKCE---EAGECPYQVSLPPL-----TIQ--LPKQFSRIEEVFKEVQN 84
 DB 26 MDSIGKKQYQVHGSCSYTFLLPEMNCSSSSSPYVSNVAVQDAPLEYDSDVQRLOVLEN 85
 QY 35 LKE-----IVNSLKSCQCKLOADNCGPGRNGLLPSTGAPGEVDN---- 128
 DB 86 IMENNTQWLKLENYIQDNKKEMVEIQQNAVQN-----QTAVMIEGTNLNC 134
 QY 129 -----RVRELESEV-----NKLSELKNAAKEEINVJHGR---LEKL 161
 DB 135 TAQTRKLTDEVAQVLNQTTRLEQLLEHSLSTNKLEKQLDQTSINKLQDKNSFLEKK 194
 QY 162 NLV-----NMNIENYVDSKVANLTF-----V 183
 DB 195 VLAMEDKHIIQLOSIKEEKQQLVLSKQNSIIEELEKXIVTATVNSVLQKQCHLMET 254
 QY 184 VNSLDGKSKCPSQEQICSRPVQHLLIYKDCSDYYAIGKRSSEYRYVTPDPKSSFEVYCD 243
 DB 255 VNNLLTMMSTNSAKDPTVAKEQISFRDCAEVFKSGHTNGTYTJTFNSEEIKAYCD 314
 QY 244 VETMGGGWTVLQARLDGSGTNFTRTWQDYKAGFGLNRREFWLNCKIHLTKSKEMILRID 303

Db 315 MEAGGGWTIIQRREDGSDVDFQRTWKYKVGFGNPSGEYWLGNFEVSQLTNQRYVLKIH 374

Qy 304 LEDFNGVELYALDYQFYVANEFLKYLHVGUNYKGTAGDARFNKYNHDLKFTTPEKON 363

Db 375 LKOWEGNEAYSLEYEHFYLSEELNRYIHLKGLTGTAAGISS-SQPGND----FSTKDGDN 430

Qy 364 DRYPSGNGCLYSSQWMEFACLSANLNGKYHCKYRGVR-NGIPNGTWPGVSEAHFGGYK 422

Db 431 DKCIC-KCSQMLTGMWFDACGSPNLNGMYPCRONTKFNGIKWYWKG-----SGY- 482

Qy 423 SSFKEAKMIRPKHF 437

Db 483 SLKATTMMIRPADF 496

RESULT 12

ID ABP58064 standard; Protein: 496 AA.

AC ABP58064;

XX

DT 07-MAR-2003 (first entry)

DE Human angiotensin-2.

XX

KW Gene therapy; vector; hepatitis B virus; cardiovascular disease;

KW heart; cardiatic; vasotropic; antiarrhythmic; antiarteriosclerotic;

KW human; angiotensin-2.

CS Homo sapiens.

XX

EN WC2020287594-A1.

XX

PC 07-NOV-2002.

XX

PF 30-APR-2002; 2002WC-US13644.

XX

PR 30-APR-2001; 2001US-267423P.

XX

PA (REGC) UNIV CALIFORNIA.

XX

PI Chien KR, Hoshijima M;

XX

DR WPI; 2003-111844/10.

XX

XX

PT Novel non-viral vector comprises vesicular membrane with hepatitis B

PT envelope protein with cardiac targeting sequence, and nucleotide

PT sequence for gene therapy useful for treating, e.g., heart failure,

PT arrhythmia and atherosclerosis.

XX

PS Disclosure; Page 38-40; 53pp; English.

XX

CC The present sequence is the protein sequence of human

CC angiotensin-2. The invention provides a non-viral vesicle vector

CC for the delivery of nucleic acid to various cardiac cell types.

CC The vesicle vector contains the hepatitis B virus envelope protein

CC in which at least part of the liver targeting sequence is deleted

CC and replaced with a specific cardiac cell targeting sequence. For

CC example, to selectively target vascular endothelial cells, peptides

CC including angiotensin-2 are used. The vesicle vector can be

CC delivered intravenously or intra-arterially rather than by more

CC invasive methods such as direct cardiac injection. It can be used

CC to deliver gene products to replace or enhance expression of

CC proteins for treatment of heart failure, arrhythmia, reperfusion

CC injury, atherosclerosis, to promote angiogenesis, etc. The vesicles

CC are highly stable and can be produced in large quantities, making

CC them ideal for gene therapy.

XX

SQ Sequence 496 AA;

Query Match 22.0%; Score 522; DB 24; Length 436;

Best Local Similarity 27.9%; Pred. No. 5.2e-38;

Matches 138; Conservative 74; Mismatches 159; Indels 124; Gaps 15;

Qy 43 LBSRGKCE---EAGECPYQVSLPPL-----TIQ---LPKQFSRIEVEFKEVQN 84

Db 26 MDSIGKKQYQVHGSCSYTFLPEMDNCRSSSPYVSNVQVADPLEYDDSVQRLQVLEN 85

Qy 85 LKE-----IVNSLKSCQCKLQADNDGPGRNGLLLPSTGAPGEVGN---- 128

Db 86 IMENNTQWLKLENYIQDNKKEMWIQKAVQN-----QTAVMIEIGTNLLNQ 134

Qy 129 -----RVRELESEV-----NKLSELKNAKEEINVHLHGR---LEKL 161

Db 135 TAFOTRKLTDVEAQLNQTTRELEQLLEHSLSTNKLKQ-LDQTSINKLQDKNSFLEKK 194

Qy 162 NJV-----NMNINIENYVDSKVANLTF-----V 183

Db 195 VLAVEDKHIIQOSIKEEKDQLOLVSKQKSI-EBLEKKIVTATVNSVLQKQCHDLMET 254

Qy 184 VNSLDGKCKSPQCEQIQSRPVOHLVYKQCSDYAIGKRSSETYRVTPDPKNSFEVYCD 243

Db 255 VKNLLTMWSTNSAKQPTVAKEEQISFRDCAEVFKSGHTTNGIYTLTFPNSTEEIKAYCD 314

Qy 244 METYGGGWTVLQARLDGSTNFTTWQDYKAGPNLRREFWLGNDKIHLITKSEMILRID 303

Db 315 MEAGGGWTIIQRREDGSDVDFQRTWKYKVGFGNPSGEYWLGNFEVSQLTNQRYVLKIH 374

Qy 304 LEDFNGVELYALDYQFYVANEFLKYLHVGUNYKGTAGDARFNKYNHDLKFTTPEKON 363

Db 375 LKOWEGNEAYSLEYEHFYLSEELNRYIHLKGLTGTAAGISS-SQPGND----FSTKDGDN 430

Qy 364 DRYPSGNGCLYSSQWMEFACLSANLNGKYHCKYRGVR-NGIPNGTWPGVSEAHFGGYK 422

Db 431 DKCIC-KCSQMLTGMWFDACGSPNLNGMYPCRONTKFNGIKWYWKG-----SGY- 482

Qy 423 SSFKEAKMIRPKHF 437

Db 483 SLKATTMMIRPADF 496

RESULT 13

ID ARG06771 standard; Protein: 572 AA.

XX

AC ARG06771;

XX

DT 13-FEB-2002 (first entry)

XX

DE Novel human diagnostic protein #6762.

XX

KW Human; chromosome mapping; gene mapping; gene therapy; forensic;

KW food supplement; medical imaging; diagnostic; genetic disorder.

XX

OS Homo sapiens.

XX

PN WO200175067-A2.

XX

PD 11-OCT-2001.

XX

PP 30-MAR-2001; 2001WO-US08631.

XX

PR 31-MAR-2000; 2000US-0540217.

XX

PR 23-AUG-2000; 2000US-0649167.

XX

XX (HYSE-) HYSEQ INC.

PA Drmanac RT, Liu C, Tang YT;

PI WP; 2001-639362/73.

XX

DE N-PSDB; AAS70958.

XX

PT New isolated polynucleotide and encoded polypeptides, useful in

PT diagnostics, forensics, gene mapping, identification of mutations

PT responsible for genetic disorders or other traits and to assess

PT biodiversity.

```
XX PS Claim 20; SEQ ID No 37133; 103pp; English.
XX CC The invention relates to isolated polynucleotide (I) and
XX CC polypeptide (II) sequences. (I) is useful as hybridisation probes,
XX CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome
XX CC and gene mapping, and in recombinant production of (II). The
XX CC polynucleotides are also used in diagnostics as expressed sequence tags
XX CC for identifying expressed genes. (II) is useful in gene therapy techniques
XX CC to restore normal activity of (II) or to treat disease states involving
XX CC (II). (II) is useful for generating antibodies against it, detecting or
XX CC quantitating a polypeptide in tissue, as molecular weight markers and as
XX CC a food supplement. (II) and its binding partners are useful in medical
XX CC imaging of sites expressing (II). (I) and (II) are useful for treating
XX CC disorders involving aberrant protein expression or biological activity.
XX CC The polypeptide and polynucleotide sequences have applications in
XX CC diagnostics, forensics, gene mapping, identification of mutations
XX CC responsible for genetic disorders or other traits to assess biodiversity
XX CC and to produce other types of data and products dependent on DNA and
XX CC amino acid sequences. ABG00010-ABG30377 represent novel human
XX CC diagnostic amino acid sequences of the invention.
XX CC Note: The sequence data for this patent did not appear in the printed
XX CC specification, but was obtained in electronic format directly from WIPO
XX CC at ftp.wipo.int/pub/published_pct_sequences.
XX SQ Sequence 572 AA;
XX Query Match 22.0%; Score 522; DB 22; Length 572;
XX Best Local Similarity 27.9%; Pred. No. 6.5e-18;
XX Matches 138; Conservative 74; Mismatches 159; Indels 124; Gaps 15;
QY 43 LBSRGKCE---FAGECPYQVSLPPL-----TIC--LPKQSRBEVEFKVQN 84
DB 102 MDSIGKQYQVCHGSCSYTFLLPEMDNCRSSSPYVSNVAVQDAPLEDDSVQRLQVLN 161
QY 85 LKE-----IVNSLKSCQDCKQADNGDPPGRNGLLLPSTGAPGEVGN--- 128
DB 162 IMENNTQWLKLENIYQDNMKKEVYEQNAVQN-----QTAVMEIGTNLLNQ 213
QY 129 -----RVRELESEV-----NKLSELKNAKEEINVHLGR---LEKL 161
DB 211 TAEQTRKLTQDVEAQLNQTTRLEQLLHSLSTNKLKQILDQTSINKLQDKNSFLEKK 270
QY 162 NLV-----NQNENYVYDCKVANLTF-----V 183
DB 271 VLAMEDKH:IQLQS:KEEKQDQGLVYSKQNSHIEELEKKIVTATVNSVLQXQOHDLMET 330
QY 184 VNSLDGKCKSPSQEQIQSRPVQHLVYKDCSDYYA:GKSSSEYRVTDPKNSFPEVYCD 243
DB 331 VNLLTMNSTNSAKDPTVAKESQISFRCAEVFKSGHTNGIYLTLPNSTEEIKAVYCD 390
QY 244 METMGGWTVLQARLDGSTNFTRTWQYAGFQNLRRBFJGJGNK:HLITKSKN:LRID 303
DB 391 MEAGGGGWIIQRPEDGVDFTQTKWEYKVGFGNPGSGEVLGNFYSQLTNSCKRYVLKIH 450
QY 304 LEDFNGVELYLDQFYVANEFLKYP:HVGNVNGTASDALRKNKYNHDLKFTTPDKN 363
DB 451 LKQWEGNEAYSLYHEFYLSSEELNYR:HLKGLGTAGK:SSISQPGND----FSTKDGKN 505
QY 364 DRYPSNGCGLYYSSGKWFDA:SANLNGKYHYKYGVR:NG:FWGTQVGVSEAHPPGYK 422
DB 507 DKIC:KCSQMLTGGKWFDA:CGFSNLNGYYPORNTN:KFNIGKYYWKG-----SGV 558
QY 423 SSFKEAKMIRPPKH 437
DB 559 -SLKATTMIRPADF 572
XX RESULT 14
XX IC ABG11614
XX XX ABG11614 standard; Protein; 1033 AA.
XX AC ABG11614;
XX DT 18-FEB-2002 (first entry)
XX DE Novel human diagnostic protein #11605.
XX KY Human; chromosome mapping; gene mapping; gene therapy; forensic;
XX KY food supplement; medical imaging; diagnostic; genetic disorder.
XX JS Homo sapiens.
XX FN W0200175567-A2.
XX PD 11-OCT-2001.
XX PF 30-MAR-2001; 2001WO-US08631.
XX PR 31-MAR-2000; 2000US-0540217.
XX PR 23-AUG-2000; 2000US-0649167.
XX XX (HYSE-) HYSEQ INC.
XX FA Dmanac Rt, Liu C, Tang YT;
XX PI WPI: 2001-639362/73.
XX DR N-PSDB; AAS7580.
XX XX New isolated polynucleotide and encoded polypeptides, useful in
XX PT diagnostics, forensics, gene mapping, identification of mutations
XX PT responsible for genetic disorders or other traits and to assess
XX PT biodiversity -
XX PS Claim 20; SEQ ID No 41973; 103pp; English.
XX CC The invention relates to isolated polynucleotide (I) and
XX CC polypeptide (II) sequences. (I) is useful as hybridisation probes,
XX CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome
XX CC and gene mapping, and in recombinant production of (II). The
XX CC polynucleotides are also used in diagnostics as expressed sequence tags
XX CC for identifying expressed genes. (II) is useful in gene therapy techniques
XX CC to restore normal activity of (II) or to treat disease states involving
XX CC (II). (II) is useful for generating antibodies against it, detecting or
XX CC quantitating a polypeptide in tissue, as molecular weight markers and as
XX CC a food supplement. (II) and its binding partners are useful in medical
XX CC imaging of sites expressing (II). (I) and (II) are useful for treating
XX CC disorders involving aberrant protein expression or biological activity.
XX CC The polypeptide and polynucleotide sequences have applications in
XX CC diagnostics, forensics, gene mapping, identification of mutations
XX CC responsible for genetic disorders or other traits to assess biodiversity
XX CC and to produce other types of data and products dependent on DNA and
XX CC amino acid sequences. ABG00010-ABG30377 represent novel human
XX CC diagnostic amino acid sequences of the invention.
XX CC Note: The sequence data for this patent did not appear in the printed
XX CC specification, but was obtained in electronic format directly from WIPO
XX CC at ftp.wipo.int/pub/published_pct_sequences.
XX SQ Sequence 1033 AA;
XX Query Match 22.0%; Score 522; DB 22; Length 1033;
XX Best Local Similarity 27.9%; Pred. No. 1.6e-37;
XX Matches 139; Conservative 74; Mismatches 159; Indels 124; Gaps 15;
QY 43 LBSRGKCE---FAGECPYQVSLPPL-----TIC--LPKQSRBEVEFKVQN 84
DB 563 MDSIGKQYQVCHGSCSYTFLLPEMDNCRSSSPYVSNVAVQDAPLEDDSVQRLQVLN 622
QY 85 LKE-----IVNSLKSCQDCKQADNGDPPGRNGLLLPSTGAPGEVGN--- 128
DB 623 IMENNTQWLKLENIYQDNMKKEVYEQNAVQN-----QTAVMEIGTNLLNQ 672
QY 129 -----RVRELESEV-----NKLSELKNAKEEINVHLGR---LEKL 161
DB 672 TAEQTRKLTQDVEAQLNQTTRLEQLLHSLSTNKLKQILDQTSINKLQDKNSFLEKK 731
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QY 162 NLV-----NNMNIVVDSKVANLT-----V 183
 DB 732 VLAMEDKHIIQOSIKKEKQOQVLVSKNSIIELEKXIVATVNVSVLQKQCHLMET 791
 QY 184 VNSLDGKSKCPSQEQIOQRPPVCHLIYKDCSDYVAIGKRSSSETYRVTDPKNSSEVYCD 243
 DB 792 VNNLLTWKSTNSAKDPTVAKESQISFRDCAEVFXSGHTNGIYLTLPNSKEEIKAYCD 551
 QY 244 METMGGWTVLQARLDGSTNFTWCDYKAGFGNLRBFWLGNDKIHLLTKSKEMILRID 303
 DB 852 MEAGGGWITIQRRDGSVDFTWKEKVGFGNPSGEYWLGNFVSLTNQQRVULKIH 911
 QY 354 LEDFNGVELYALYDQFYVANEELKYLRLHVGKYNGTAGDALRKNKYNHDLKEFTFDKON 363
 DB 912 LKDWEGNEAYSLEYFYSSSEELKYRIHLKGTGTAGKISS-SQPGND----FSTKDGK 967
 QY 364 DRYPGNGCLYSSGWKFDACLSANLNGKYYHCKYRGYR-NGIFWGTWPGVSEAHFGGYK 422
 DB 968 DKCIC-KSQMLTGSWFDACGSPSNLNGMYYPQONTNKFNGIKWYKKG-----SGY- 1019
 QY 423 SFFKXAKXMMIRPKHF 437
 DB 1020 -SLKATTMIRPADF 1033

RESULT 15

ID AAW47528 standard; Protein; 498 AA.

AC AAW47528;

DT 09-SEP-1998 (first entry)

DE Amino acid sequence of chimeric TIE ligand IN1C2F (chimera 1).

KW Chimeric TIE ligand IN1C2F; TIE-2 ligand; neovascularisation;
 tumour; human.

OS Homo sapiens.

PN W09805779-A1.

PD 12-FEB-1998.

PF 01-AUG-1997; 9FWO-US13557.

XX 25-OCT-1996; 96US-0740223.

FR 02-AUG-1996; 96US-0222999.

PA (REG-) REGENERON PHARM. INC.

XX Davis S, Yancopoulos GD;

XX MPI; 1998-145615/13.

DR N-PSDB; AAV18615.

XX Modified human TIE-2 receptor ligand(s) - useful for promoting wound
 healing

XX Claim 20; Fig 24; 202pp; English.

CC This is the amino acid sequence of the chimeric TIE ligand IN1C2F,
 used in the method of the invention, involving the production
 of TIE-2 ligands which promote healing. The nucleic acids, vectors
 and host cells used in the method of the invention are useful for
 the recombinant production of the ligands. The ligands, etc. are
 useful for blocking blood vessel growth, promoting neovascularisation,
 promoting the growth or differentiation of a cell expressing the TIE
 receptor, blocking the growth or differentiation of a cell expressing
 the TIE receptor and for attenuating or preventing tumour growth in
 a human.

XX Sequence 498 AA;

Query Match 21.9%; Score 521.5; DB 19; Length 498;
 Best Local Similarity 32.7%; Pred. No. 5.8e-38;
 Matches 131; Conservative 61; Mismatches 138; Indels 7; Gaps 14;
 QY 61 LPPLTIOLPKQFSRIE-----EVPKEVQNLEKEIVNSLKSCDCKLOADENGDPGRN 112
 DB 145 LTVETQVLTQTRLEQLLENLSLYKLEKQLQQTNEILKIH-----KN 191
 QY 113 GLLLPSTGAPGEVDNRVRESEVNKLSSELKNKAKEEINVLRG-----RLK-L 161
 DB 192 SLL-----EKKILEMS--GKKEELDTLKEKENLOGLVTRQYIIOLEKQL 237
 QY 162 NVMNMNIENVDSKVANLTFFVNSLDGKSK-----CPSEQIQSRPVQHLIYKDCSDY 217
 DB 238 NRATTNN--SVLQKQQJELMDTYHNLVNLCTKRGVLLKGGKREEKP-----PRDCAEVF 290
 QY 218 AIGKRSETYRVTDPKNSSEVYVCDMETWGGWTVLQARLDGSTNFTRTWODYKAGFGN 277
 DB 291 KSGHTTNGIYLTLPNSKEEIKAYCDMEAGGGWITIQRRDSSVDFTWKEYKVGFGN 350
 QY 278 LRREFWLGNDKIHLLTKSKEMILRIDLEDFNGVELYALYDQFYVANEFLKYRLHVGNYNG 337
 DB 351 PSGEYWLGNFVSLTNQQRVULKIHLKDWEGNEAYSLEYDLYLSSEELNRYRIHLKGLTG 410
 QY 338 TAGDALRKNKYNHDLKXFTTPKDNDRYPSGNGCLYSSGWKFDACLSANLNGKYYHOK 397
 DB 411 TAGKISSISQPGND----FSTKGDNDKIC-KSQMLTGSWFDACGSPSNLNGMYYPQR 465
 QY 398 YRGYR-NGIFWGTWPGVSEAHFGGYKSSFKXAKXMMIRPKHF 437
 DB 466 QNTNKFNGIKWYKKG-----SGY--SLKATTMIRPADF 498

Search completed: November 5, 2003, 16:45:59

Job time : 100.359 secs

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OM protein - protein search, using sw model

Run on: November 5, 2003, 16:48:06 ; Search time 49.315 Seconds
(without alignments)
1528.905 Million cell updates/sec

Title: US-09-902-563-2

Perfect score: 2378

Sequence: 1 MCLANWYWLSSAVLATYGFVANNETEEIKDERAKDVCVRLSESGKCEEGECYPQVS

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 644079 seqs, 171749292 residues

Total number of hits satisfying chosen parameters: 644079

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA.*

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2: /cgn2_6/prodata/2/pubpaa/CT_NEW_PUB.pep.*
3: /cgn2_6/prodata/2/pubpaa/US06_NEW_PUB.pep.*
4: /cgn2_6/prodata/2/pubpaa/US06_PUBCOMB.pep.*
5: /cgn2_6/prodata/2/pubpaa/US07_NEW_PUB.pep.*
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15: /cgn2_6/prodata/2/pubpaa/US10C_PUBCOMB.pep.*
16: /cgn2_6/prodata/2/pubpaa/US10_NEW_PUB.pep.*
17: /cgn2_6/prodata/2/pubpaa/US60_NEW_PUB.pep.*
18: /cgn2_6/prodata/2/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2378	100.0	439	11	US-09-902-563-2
2	2378	100.0	439	11	US-10-C96-255-2
3	1853.5	77.9	432	11	US-09-902-563-4
4	1853.5	77.9	432	15	US-10-C96-255-4
5	525	22.1	496	15	US-10-263-677-9
6	524	22.0	496	15	US-10-215-224-7
7	522	22.0	480	15	US-10-225-060-8
8	522	22.0	496	10	US-09-998-831-4
9	522	22.0	496	10	US-09-997-306-14
10	522	22.0	496	12	US-10-136-939-13
11	522	22.0	496	12	US-10-179-615-6
12	522	22.0	496	12	US-10-179-820-6
13	522	22.0	496	12	US-10-373-563-4
14	522	22.0	496	14	US-10-179-744-6
15	522	22.0	496	14	US-10-179-744-6

16	522	22.0	496	15	US-10-186-817-6	Sequence 6, Appli
17	522	22.0	496	15	US-10-215-224-8	Sequence 8, Appli
18	522	22.0	496	15	US-10-225-060-6	Sequence 6, Appli
19	522	22.0	496	15	US-10-263-677-8	Sequence 8, Appli
20	522	22.0	496	15	US-10-321-332-6	Sequence 20, Appli
21	521.5	21.9	498	15	US-10-225-060-20	Sequence 20, Appli
22	517.5	21.8	499	15	US-10-225-060-24	Sequence 24, Appli
23	510	21.4	496	15	US-10-225-060-15	Sequence 15, Appli
24	506	21.3	339	9	US-09-925-301-1082	Sequence 1082, Ap
25	505	21.2	491	10	US-09-997-306-1	Sequence 1, App-i
26	505	21.2	491	12	US-10-137-870-278	Sequence 278, App
27	505	21.2	491	12	US-10-140-018-278	Sequence 278, App
28	505	21.2	491	12	US-10-140-021-278	Sequence 278, App
29	505	21.2	491	12	US-10-140-274-278	Sequence 278, App
30	505	21.2	491	12	US-10-140-471-278	Sequence 278, App
31	505	21.2	491	12	US-10-140-807-278	Sequence 278, App
32	505	21.2	491	12	US-10-140-922-278	Sequence 278, App
33	505	21.2	491	12	US-10-140-924-278	Sequence 278, App
34	505	21.2	491	12	US-10-140-926-278	Sequence 278, App
35	505	21.2	491	12	US-10-141-698-278	Sequence 278, App
36	505	21.2	491	12	US-10-141-702-278	Sequence 278, App
37	505	21.2	491	12	US-10-141-704-278	Sequence 278, App
38	505	21.2	491	12	US-10-142-421-278	Sequence 278, App
39	505	21.2	491	12	US-10-142-432-278	Sequence 278, App
40	505	21.2	491	12	US-10-142-767-278	Sequence 278, App
41	505	21.2	491	12	US-10-143-033-278	Sequence 278, App
42	505	21.2	491	12	US-10-144-994-278	Sequence 278, App
43	505	21.2	491	12	US-10-145-628-278	Sequence 278, App
44	505	21.2	491	12	US-10-145-631-278	Sequence 278, App
45	505	21.2	491	12	US-10-145-633-278	Sequence 278, App

ALIGNMENTS

RESULT 1
US-09-902-563-2
; Sequence 2, Application US/09902563
; Publication No. US20030095654A1
; GENERAL INFORMATION:
; APPLICANT: Levy, Gary
; TITLE OF INVENTION: Methods of Modulating Immune Coagulation
; FILE REFERENCE: 9579-37
; CURRENT APPLICATION NUMBER: US/09/902,563
; CURRENT FILING DATE: 2002-09-03
; PRIOR APPLICATION NUMBER: US 09/442,143
; PRIOR FILING DATE: 1999-11-15
; NUMBER OF SEQ ID NOS: 53
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 439
; TYPE: PRT
; ORGANISM: Homo sapiens fgl2
US-09-902-563-2

Query Watch	100.0%	Score 2378	DB 11	Length 439
Best Local Similarity	100.0%	Pred. No. 1.4e+207		
Matches 439	Conservative 0	Mismatches 0	Indels 0	Gaps 0
QY	1	MCLANWYWLSSAVLATYGFVANNETEEIKDERAKDVCVRLSESGKCEEGECYPQVS	60	
DB	1	MCLANWYWLSSAVLATYGFVANNETEEIKDERAKDVCVRLSESGKCEEGECYPQVS	60	
QY	61	LPPTIOLPQFGRIBEVFKEVQNLKEIVNSLKSCODCKLOADDNGDPGRNGLLPSTG	120	
DB	61	LPPTIOLPQFGRIBEVFKEVQNLKEIVNSLKSCODCKLOADDNGDPGRNGLLPSTG	120	
QY	121	APGEGVGNRVRELESEVKNLSSELKKAKEEINVHGRLEKLNLVNKNENYVDSKVANL	180	
DB	121	APGEGVGNRVRELESEVKNLSSELKKAKEEINVHGRLEKLNLVNKNENYVDSKVANL	180	
QY	181	TFVNSLDGKCKPCPSQEQIOSRPVQHLIYKQSDYYAIGKRSSEYRYVTPDPKNSSEFV	240	


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Db 181 TFVNSLDGKCKSCPSQEQIQSRPVQHLYKDCSDYYAIGKRSSSETYRVTPDPKNSSEFV 240
Qy 241 YCDMETMGSGWTVLQARLDGSGNFTRTWQDYKAGFGLNLRREFWLGNDKIHLLTKSKEMIL 300
Db 241 YCDMETMGSGWTVLQARLDGSGNFTRTWQDYKAGFGLNLRREFWLGNDKIHLLTKSKEMIL 300
Qy 301 RIDLEDNGVELYALYDQFYVANEFLKYRLHVGNYNGTAGDALRPNKHVNDLKFETTPD 360
Db 301 RIDLEDNGVELYALYDQFYVANEFLKYRLHVGNYNGTAGDALRPNKHVNDLKFETTPD 360
Qy 361 KNDRYPSGNGCLYYSSGWWFDCLSANLNGKYHQQYKRGVNGIFWGTWPGVSEAHPGG 420
Db 361 KNDRYPSGNGCLYYSSGWWFDCLSANLNGKYHQQYKRGVNGIFWGTWPGVSEAHPGG 420
Qy 421 YKSFKEAKMIRPKFKP 439
Db 421 YKSFKEAKMIRPKFKP 439

RESULT 2
US-10-096-255-2
; Sequence 2, Application US/10096255
; Publication No. US20030103974A;
; GENERAL INFORMATION:
; APPLICANT: Levy, Gary
; APPLICANT: Clark, David A.
; TITLE OF INVENTION: Methods of Modulating Immune Coagulation
; FILE REFERENCE: 9579-52
; CURRENT APPLICATION NUMBER: US/10/096,255
; PRIOR FILING DATE: 2002-03-13
; PRIOR FILING DATE: 1997-05-17
; PRIOR APPLICATION NUMBER: US 60/046,537
; PRIOR APPLICATION NUMBER: US 60/061,684
; PRIOR FILING DATE: 1997-10-10
; NUMBER OF SEQ ID NOS: 53
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 439
; TYPE: PRT
; ORGANISM: Homo sapiens fg-2
US-10-096-255-2

Query Match 100.0%; Score 2378; DB 15; Length 439;
Best Local Similarity 100.0%; Pred No. 1 4e-207;
Matches 439; Conservative 3; Mismatches 3; Indels 3; Gaps 0;

Qy 1 MKLAWYWLSSAVLATYGFVLVANNTEETIKDERAKDVCPVRLSRGKCEEGECPCYQVS 60
Db 1 YKLAWYWLSSAVLATYGFVLVANNTEETIKDERAKDVCPVRLSRGKCEEGECPCYQVS 60
Qy 61 LPPLTIQLPKQFSRIEVEVFKEVQNLKEIVNSLKKSCDCKLQADDNGDPGRNGLLLPSTG 120
Db 61 LPPLTIQLPKQFSRIEVEVFKEVQNLKEIVNSLKKSCDCKLQADDNGDPGRNGLLLPSTG 120
Qy 121 APGEVDNRVRESEVSEVKNLSSELKNAAKEEINVLRHGRLEKLNVMNNIENYVDSKVANL 180
Db 121 APGEVDNRVRESEVSEVKNLSSELKNAAKEEINVLRHGRLEKLNVMNNIENYVDSKVANL 180
Qy 181 TFVNSLDGKCKSCPSQEQIQSRPVQHLYKDCSDYYAIGKRSSSETYRVTPDPKNSSEFV 240
Db 181 TFVNSLDGKCKSCPSQEQIQSRPVQHLYKDCSDYYAIGKRSSSETYRVTPDPKNSSEFV 240
Qy 241 YCDMETMGSGWTVLQARLDGSGNFTRTWQDYKAGFGLNLRREFWLGNDKIHLLTKSKEMIL 300
Db 241 YCDMETMGSGWTVLQARLDGSGNFTRTWQDYKAGFGLNLRREFWLGNDKIHLLTKSKEMIL 300
Qy 301 RIDLEDNGVELYALYDQFYVANEFLKYRLHVGNYNGTAGDALRPNKHVNDLKFETTPD 360
Db 301 RIDLEDNGVELYALYDQFYVANEFLKYRLHVGNYNGTAGDALRPNKHVNDLKFETTPD 360
Qy 361 KNDRYPSGNGCLYYSSGWWFDCLSANLNGKYHQQYKRGVNGIFWGTWPGVSEAHPGG 420
Db 361 KNDRYPSGNGCLYYSSGWWFDCLSANLNGKYHQQYKRGVNGIFWGTWPGVSEAHPGG 420

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Qy 421 YKSFKEAKMIRPKFKP 439
Db 421 YKSFKEAKMIRPKFKP 439

RESULT 3
US-09-902-563-4
; Sequence 4, Application US/0992563
; Publication No. US2003009654A1
; GENERAL INFORMATION:
; APPLICANT: Levy, Gary
; APPLICANT: Clark, David A.
; TITLE OF INVENTION: Methods of Modulating Immune Coagulation
; FILE REFERENCE: 9579-37
; CURRENT APPLICATION NUMBER: US/09/902,563
; CURRENT FILING DATE: 2002-09-09
; PRIOR APPLICATION NUMBER: US 09/442,143
; PRIOR FILING DATE: 1999-11-15
; NUMBER OF SEQ ID NOS: 53
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 432
; TYPE: PRT
; ORGANISM: Murine fg12
US-09-902-563-4

Query Match 77.9%; Score 1853.5; DB 11; Length 432;
Best Local Similarity 77.7%; Pred No. 6.7e-160;
Matches 341; Conservative 42; Mismatches 49; Indels 7; Gaps 4;

Qy 1 MKLAWYWLSSAVLATYGFVLVANNTEETIKDERAKDVCPVRLSRGKCEEGECPCYQVS 60
Db 1 YKLAWYWLSSAVLATYGFVLVANNTEETIKDERAKDVCPVRLSRGKCEEGECPCYQVS 60
Qy 61 LPPLTIQLPKQFSRIEVEVFKEVQNLKEIVNSLKKSCDCKLQADDNGDPGRNGLLLPSTG 120
Db 61 LPPLTIQLPKQFSRIEVEVFKEVQNLKEIVNSLKKSCDCKLQADDNGDPGRNGLLLPSTG 120
Qy 121 APGEVDNRVRESEVSEVKNLSSELKNAAKEEINVLRHGRLEKLNVMNNIENYVDSKVANL 180
Db 121 APGEVDNRVRESEVSEVKNLSSELKNAAKEEINVLRHGRLEKLNVMNNIENYVDSKVANL 180
Qy 181 TFVNSLDGKCKSCPSQEQIQSRPVQHLYKDCSDYYAIGKRSSSETYRVTPDPKNSSEFV 240
Db 181 TFVNSLDGKCKSCPSQEQIQSRPVQHLYKDCSDYYAIGKRSSSETYRVTPDPKNSSEFV 240
Qy 241 YCDMETMGSGWTVLQARLDGSGNFTRTWQDYKAGFGLNLRREFWLGNDKIHLLTKSKEMIL 300
Db 241 YCDMETMGSGWTVLQARLDGSGNFTRTWQDYKAGFGLNLRREFWLGNDKIHLLTKSKEMIL 300
Qy 301 RIDLEDNGVELYALYDQFYVANEFLKYRLHVGNYNGTAGDALRPNKHVNDLKFETTPD 360
Db 301 RIDLEDNGVELYALYDQFYVANEFLKYRLHVGNYNGTAGDALRPNKHVNDLKFETTPD 360
Qy 361 KNDRYPSGNGCLYYSSGWWFDCLSANLNGKYHQQYKRGVNGIFWGTWPGVSEAHPGG 420
Db 361 KNDRYPSGNGCLYYSSGWWFDCLSANLNGKYHQQYKRGVNGIFWGTWPGVSEAHPGG 420
Qy 421 YKSFKEAKMIRPKFKP 439
Db 421 YKSFKEAKMIRPKFKP 439

RESULT 4
US-10-096-255-4
; Sequence 4, Application US/10096255
; Publication No. US20030103974A1
; GENERAL INFORMATION:
; APPLICANT: Levy, Gary
; APPLICANT: Clark, David A.
; TITLE OF INVENTION: Methods of Modulating Immune Coagulation
; FILE REFERENCE: 9579-52
; CURRENT APPLICATION NUMBER: US/10/096,255

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; CURRENT FILING DATE: 2002-03-13
; PRIOR APPLICATION NUMBER: US 60/046,537
; PRIOR FILING DATE: 1997-05-17
; PRIOR APPLICATION NUMBER: US 60/061,684
; PRIOR FILING DATE: 1997-10-10
; NUMBER OF SEQ ID NOS: 53
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 432
; TYPE: PRT
; ORGANISM: Murine fgl2
US-10-096-255-4

Query Match 77.9%; Score 1853.5; DB 15; Length 432;
Best Local Similarity 77.7%; Pred. No. 6.7e-160;
Matches 341; Conservative 42; Mismatches 49; Indels 7; Gaps 4;
QY 1 MKLANWYLSAVLATYGFVAVNNEETETIKERAKDVPVRLBSRGKCEAGCEGCPYQVS 60
DB 1 MRLPGWLWSSAVLAACR-AVEEHNLTGLEDSAAQA-CPARLEGGRC-EGSCPPFLT 58
QY 61 LPPJTTLQPKQFSRIEEVFKEVQNLEKEIVNSLKKSCQCKLOADMGPGRNG-LLPSTG 120
DB 59 LPTJTLQPKQFSRIEEVFKEVQNLEKEIVNSLKKSCQCKLOADMGPGRNG-LLPSTG 114
QY 121 APGEVGDNRVRELESEVKNLSSELKNAKEEINVJHGR-EKLNLYNNANIENYVSKVANL 120
DB 115 AE-TAEDSRVQLESQVKNLSSELKNAKEEINVJHGR-EKLNLYNNANIENYVSKVANL 173
QY 181 TFWANSLDGKCKSPQEQIQSRPVOHLIYKDCSDYVAIGKRSSTYRTVTPDPKNSFEV 240
DB 174 TFWANSLDGKCKSPQEQIQSRPVOHLIYKDCSDYVAIGKRSSTYRTVTPDPKNSFEV 233
QY 241 YCDMETMGSGTVLQARLDGSGTNFTRTWQDYKAGFNGNLRREFWLNCKIHLTKSEVIL 300
DB 234 YCDMETMGSGTVLQARLDGSGTNFTRTWQDYKAGFNGNLRREFWLNCKIHLTKSEVIL 293
QY 301 RIDLEDFNGVELYALYDQFYVANEFLKYRLHVGNYNGTAGDALRFNKHYNHDLKFTTTPD 360
DB 294 RIDLEDFNGVELYALYDQFYVANEFLKYRLHVGNYNGTAGDALRFNKHYNHDLKFTTTPD 353
QY 361 KNDRYPSGNCGLYSSGWMFDACLSANLNGKYHOKYRGVNGIFWGTWPGVSEAHPGG 420
DB 354 RNDRYPSGNCGLYSSGWMFDACLSANLNGKYHOKYRGVNGIFWGTWPGVSEAHPGG 413
QY 421 YKSSFKAKAMIRPKFKP 439
DB 414 YKSSFKAKAMIRPKFKP 432

RESULT 5
US-10-263-677-9
; Sequence 9, Application US/10263677
; Publication No. US2003009994A1
; GENERAL INFORMATION:
; APPLICANT: Holtzman, Douglas A.
; APPLICANT: Spiegelman, Bruce W.
; APPLICANT: Yoon, Clifford H.
; TITLE OF INVENTION: NOVEL PDG PROTEIN AND NUCLEIC ACID MOLECULES
; TITLE OF INVENTION: AND USES THEREOF
; FILE REFERENCE: MKI-115CP2
; CURRENT FILING DATE: 2002-10-03
; PRIOR APPLICATION NUMBER: US/09/546,547
; PRIOR FILING DATE: 2001-08-09
; PRIOR APPLICATION NUMBER: 09/261,004
; PRIOR FILING DATE: 1999-03-02
; PRIOR APPLICATION NUMBER: 09/033,539
; PRIOR FILING DATE: 1998-03-02
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 9
; LENGTH: 496

; TYPE: PRT
; ORGANISM: Mus musculus
US-10-263-677-9

Query Match 22.1%; Score 525; DB 15; Length 496;
Best Local Similarity 32.9%; Pred. No. 5.4e-39;
Matches 127; Conservative 65; Mismatches 154; Indels 40; Gaps 9;

QY 61 LPPJTTLQPKQFSRIEEVFKEVQNLEKEIVNSLKKSCQCKLOADMGPGRNG-LLPSTG 120
DB 142 LTDVEAQVLNQ-TTL-----ELQLLQHSISTNKLKLEKQILDQTS-EINKLQNKNSFL----- 191
QY 121 APGEVGDNRVRELESEVKNLSSELKNAKEEINVJHGRL-----EKLNLVNNANIENY 172
DB 192 -----EQVLDMEGRHSEGLQSMKEQKDELQVLVSKQSSVDELEKLVATVNN--SL 243
QY 173 VDSKVANLTFVWNSLDGKCKSPQEQIQSRPVOHLIYKDCSDYVAIGKRSSTYRTVTPD 232
DB 244 LQKQCHDLMETVNSLJTMNSSPNKSSVAIRKEEOTTFRDCAEIPKSGLTTSIGIYTLTFP 303
QY 233 PKNSFEVCDMETMGSGTVLQARLDGSGTNFTRTWQDYKAGFNGNLRREFWLNCKIHLTK 292
DB 304 NSTEEIKAYCDMDVGGGWTIVICHREDGSGVCFQRTWKYKEGFGNPLGEYWLGNFEVSQ 363
QY 293 TKSKEVILRIDLEDFNGVELYALYDQFYVANEFLKYRLHVGNYNGTAGDALRFNKHYNH 352
DB 364 TQGHRYVLKIQKDWGNEHAHSYDFYLAGESNYRIHLTGLTGTAAKISSSQFGSD- 422
QY 353 LKFTTTPDKNDRYPSGNCGLYSSGWMFDACLSANLNGKYHOKYRGVNR-NGIFWGTW 411
DB 423 ---FSTKDSNDKCI-C-KCSQLSGGWMFDACPSNLNGQYYPKONTNKFNGIKWYYWK 478
QY 412 GVSENPAGGYKSSFKAKAMIRPKFKP 437
DB 479 G-----SGY--SKATTNMRPADF 496

RESULT 6
US-10-215-224-7
; Sequence 7, Application US/10215224
; Publication No. US2003005987A1
; GENERAL INFORMATION:
; APPLICANT: Valenzuela et al.
; TITLE OF INVENTION: NOVEL LIGANDS, METHODS OF MAKING AND USES THEREOF
; FILE REFERENCE: REG330-K
; CURRENT APPLICATION NUMBER: US/10/215,224
; CURRENT FILING DATE: 2002-08-08
; PRIOR APPLICATION NUMBER: US/09/202,491
; PRIOR FILING DATE: 1998-11-16
; PRIOR APPLICATION NUMBER: PCT/US97/10728
; PRIOR FILING DATE: 1997-06-19
; PRIOR APPLICATION NUMBER: 60/022,999
; PRIOR FILING DATE: 1996-08-02
; PRIOR APPLICATION NUMBER: 60/021,087
; PRIOR FILING DATE: 1996-07-02
; PRIOR APPLICATION NUMBER: 08/665,926
; PRIOR FILING DATE: 1996-06-19
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 7
; LENGTH: 496
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-215-224-7

Query Match 22.0%; Score 524; DB 15; Length 496;
Best Local Similarity 32.9%; Pred. No. 6.7e-39;
Matches 127; Conservative 65; Mismatches 154; Indels 40; Gaps 9;
QY 61 LPPJTTLQPKQFSRIEEVFKEVQNLEKEIVNSLKKSCQCKLOADMGPGRNG-LLPSTG 120
DB 142 LTDVEAQVLNQ-TTL-----ELQLLQHSISTNKLKLEKQILDQTS-EINKLHKNNSFL----- 191

QY 121 APGEVDNRVRELESEVYNKLSSELKNAKEEINVLHGR-----EKLNLNNWNNLEWY 172
 Db 192 -----EOKVLCEYEGKHSQQLSMKEQKDELQVLVSKQSSVIDELERKLVTATVNN--SL 243
 QY 173 VDSKVANLTFVNSLDGKSKCPSPQICSPBPVCHLVKDCGLYVAIGKRSETVAVTPD 232
 Db 244 LKQHQHLMETVNSLLTMMSSNSKSSVAIRKEEQTTFRDCAEIPKSLTSGYTLTFP 303
 QY 233 PRNSSFVYCDMETGGGWTVJQARLDGSTNFTRMQYKAGFGLRRREFWLGKDKHLL 292
 Db 304 NSTEEIKAYCDMDVGGGWTVJQHREDGSDVDFQRTWKKEYKEGFGNPLGEYMLGREFVSQ 363
 QY 293 TSKEMILIDLEDFNGVELYALYQCFYVANFELKYLRLHVGNVNTAGDALRPNKHND 352
 Db 364 TQCHRYVLKIQLDWEGNEAHSYCHFYLAGESYRIHETGLTGTAAKSSISQPGSD- 422
 QY 353 LKPFITPDKDNDRYPGNGCLYSSGWMFDCALSNLNGKYHCKYRGVR-NGIFWGTWP 411
 Db 423 ---FSTKSDSDKIC-KCSQMLSGGWMFDCGPNLKGQYYPQONTNKNFNGIKWYYWK 478
 QY 412 GYSEAHPGGYKSPKBAQWIRPKHF 437
 Db 479 G-----SGY--SLKATTWIRPADF 496

RESULT 7

US-10-225-060-8
 ; Sequence 8, Application US/10225060
 ; Publication No. US20030092891A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Davis et al.
 ; TITLE OF INVENTION: Expressed Ligand - Vascular Inter-cellular Signaling
 ; FILE REFERENCE: REG 333-Z
 ; CURRENT APPLICATION NUMBER: US/10/225,060
 ; PRIOR FILING DATE: 2002-08-21
 ; PRIOR FILING DATE: 2000-11-09
 ; PRIOR APPLICATION NUMBER: 08/740,223
 ; PRIOR FILING DATE: 1996-10-25
 ; NUMBER OF SEQ ID NOS: 30
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 8
 ; LENGTH: 483
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-10-225-060-9

Query Match 22.0%; Score 522; DB 15; Length 480;
 Best Local Similarity 27.9%; Pred. No. 9,7e-39;
 Matches 138; Conservative 74; Mismatches 159; Indels 124; Gaps 15;

QY 43 LESRGKCE---EAGECPYQVSLPPL-----TIQ--LPKQFSRIEVPKEVQN 84
 Db 10 MDSIGKKQYQVGHGSCSYTFLLPEMNCRSSSPYVSNVQRPDALEYDSDVQRJQVLEN 69
 QY 85 LKE-----IVNSLKSCDCKLQADNGDFGNGLLPSTGAPGEVGN---- 128
 Db 70 IMENNTQWLKLENYIQDNMKEMVEIQQNAVGN-----QTAVMIEIGTNLQ 118
 QY 129 -----RVRELESEV-----NKNNIENYVDSKVANLTF-----V 183
 Db 119 TAFQTRKLTQVEAQVNLQTTRELLQLEHSLSTNKLKQILQTSSEINKLQKNSFLEK 178
 QY 162 NLV-----VLAMEDKHITLOSKEEKDQLQVLVSKQNSIIIELEKKIVTATVNNVLOKQCHDLMET 183
 Db 179 VLAMEDKHITLOSKEEKDQLQVLVSKQNSIIIELEKKIVTATVNNVLOKQCHDLMET 236
 QY 184 VNSLDGKSKCPSPQICQSRPQVQHLIYKDCSDYIYAGKRSETYRVTDPKNSSEVYCD 243
 Db 239 VNNLLTMMSTNSAKOPTVAKKEQISFRDCAEVFKSGHTINGIYTLTFPNSSTEEIKAYCD 298
 QY 244 METMGGGWTVLQARLDGSTNFTRTWQDYKAGFGLRRREFWLGKDKHLLTQSKEMILRID 303

Db 299 XEAGGGGWTIIQRRDGSVDFTQRTWKKEYKVGFGNPSGEYWLGNFVSQJTNQCRYVLK-H 358
 QY 304 LEDPFGVELYALYQCFYVANFELKYLRLHVGNVNTAGDALRPNKHYNHDLKPFITPDKEN 363
 Db 359 LKQWEGNEAHSYCHFYLAGESYRIHETGLTGTAAKSSISQPGSD----FSTKDGDN 414
 QY 364 DRYPSGNGCLYSSGWMFDCALSNLNGKYHCKYRGVR-NGIFWGTWPVSEAHPGGYK 422
 Db 415 DKIC-KCSQMLTGGGWMFDCGPNLNGMYYPQONTNKNFNGIKWYYWKG-----SGY- 466
 QY 423 SSKPKAKCMIRPKHF 437
 Db 467 -SLKATTWIRPADF 480

RESULT 8

US-09-998-831-4
 ; Sequence 4, Application US/09998831
 ; Patent No. US20020119153A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Philip E. Thorpe
 ; TITLE OF INVENTION: ANTIBODY CONJUGATE COMPOSITIONS FOR SELECTIVELY
 ; TITLE OF INVENTION: INHIBITING VEGF
 ; FILE REFERENCE: 4001.002584
 ; CURRENT APPLICATION NUMBER: US/09/998,831
 ; CURRENT FILING DATE: 2001-11-30
 ; PRIOR APPLICATION NUMBER: 09/561,108
 ; PRIOR FILING DATE: 2000-04-28
 ; NUMBER OF SEQ ID NOS: 44
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 4
 ; LENGTH: 496
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-09-998-831-4

Query Match 22.0%; Score 522; DB 10; Length 496;
 Best Local Similarity 27.9%; Pred. No. 1e-38;
 Matches 138; Conservative 74; Mismatches 159; Indels 124; Gaps 15;

QY 43 LESRGKCE---EAGECPYQVSLPPL-----TIQ--LPKQFSRIEVPKEVQN 84
 Db 26 MDSIGKKQYQVGHGSCSYTFLLPEMNCRSSSPYVSNVQRPDALEYDSDVQRJQVLEN 85
 QY 85 LKE-----IVNSLKSCDCKLQADNGDFGNGLLPSTGAPGEVGN---- 128
 Db 86 IMENNTQWLKLENYIQDNMKEMVEIQQNAVGN-----QTAVMIEIGTNLQ 134
 QY 129 -----RVRELESEV-----NKNNIENYVDSKVANLTF-----V 183
 Db 135 TAFQTRKLTQVEAQVNLQTTRELLQLEHSLSTNKLKQILQTSSEINKLQKNSFLEK 194
 QY 162 NLV-----VLAMEDKHITLOSKEEKDQLQVLVSKQNSIIIELEKKIVTATVNNVLOKQCHDLMET 254
 QY 184 VNSLDGKSKCPSPQICQSRPQVQHLIYKDCSDYIYAGKRSETYRVTDPKNSSEVYCD 243
 Db 255 VNNLLTMMSTNSAKOPTVAKKEQISFRDCAEVFKSGHTINGIYTLTFPNSSTEEIKAYCD 314
 QY 244 METMGGGWTVLQARLDGSTNFTRTWQDYKAGFGLRRREFWLGKDKHLLTQSKEMILRID 303
 Db 315 XEAGGGGWTIIQRRDGSVDFTQRTWKKEYKVGFGNPSGEYWLGNFVSQJTNQCRYVLK-H 374
 QY 304 LEDPFGVELYALYQCFYVANFELKYLRLHVGNVNTAGDALRPNKHYNHDLKPFITPDKEN 363
 Db 375 LKQWEGNEAHSYCHFYLAGESYRIHETGLTGTAAKSSISQPGSD----FSTKDGDN 430
 QY 364 DRYPSGNGCLYSSGWMFDCALSNLNGKYHCKYRGVR-NGIFWGTWPVSEAHPGGYK 422
 Db 431 DKIC-KCSQMLTGGGWMFDCGPNLNGMYYPQONTNKNFNGIKWYYWKG-----SGY- 482

QY 423 SSFKEAKMIRPKGF 437
| | | | |
Db 483 -SLKATTMIRPADF 496

RESULT 9

US-09-897-306-14
; Sequence 14, Application US/09897306
; Patent No. US20020123054A1
; GENERAL INFORMATION:
; APPLICANT: Hillman, Jennifer L.
; APPLICANT: Gorgone, Gina A.
; APPLICANT: Patterson, Chandra
; APPLICANT: Murry, Lynn E.
; TITLE OF INVENTION: HUMAN ANGIOPOIETIN
; FILE REFERENCE: PC-0048 CIP
; CURRENT APPLICATION NUMBER: US/09/897,306
; CURRENT FILING DATE: 2001-07-02
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PERL Program
; SEQ ID NO 14
; LENGTH: 496
; TYPE: PRT
; ORGANISM: Homo sapiens
; ORGANISM: Homo sapiens
US-09-897-306-14

Query Match 22.0%; Score 522; DB 10; Length 496;

Best Local Similarity 27.9%; Pred. No. 1e-38; Mismatches 159; Indels 124; Gaps 15;

Matches 138; Conservative 74; Mismatches 159; Indels 124; Gaps 15;

QY 43 LBSRGKCE---EAGCPYCVSLPPL-----TIQ--LPKQSRLEEVEKEYQN 84
| | | | |
Db 26 YDSIGKQYQVCHGSCSYTFLLPEMNCRSSSSPYVSNVAVQDAPLEYYDDSVQRLQVLEN 85
| | | | |
QY 85 LKE-----IVNSLKSCQCCQLQADDNCPGRNGLLPSTGAPREVGN----- 128
| | | | |
Db 86 INENNTQWLKLENYIQDNYKKEMVEIQONAVQN-----QTAVMIEIGTNLLNQ 134
| | | | |
QY 129 -----RVRELESEV-----NKLSELKNAKEEINVULHGR-----LEKL 161
| | | | |
Db 135 TABQTRKLTDEVAQVNLQTRLEQLLHLSLSTNKLKQILDQTSLEINKLQDNKSFLEKK 194
| | | | |
QY 162 N.V-----NMNNIENVVDSKVANLTP-----V 183
| | | | |
Db 195 VLAEXDKHIIQLOSTKEEKDQQLVLSKNSIIELEKKIVTATVNSVLQKQCHDLMET 254
| | | | |
QY 184 VNSLDGKSCPSQEQIQSRPVQHLYIKDCSDYYAIGKSSSETYRVTDPKNSSEFVYCD 243
| | | | |
Db 255 VNNLLTMSTNSAKDPTVAKEEQISPRDCAEVKSGHTNGIYTLTPNSTEELKAYCD 314
| | | | |
QY 244 METMGSGTVALQARDGSGTNFTTQDVKAGFGNLRREFWLGNDKIHLLTKSKEMILRID 303
| | | | |
Db 315 MEAGGGGTIIORREDGSDVDFQRTWKEVKVGFNGSGEYWLGNFVSQLTQQRVVLKIH 374
| | | | |
QY 304 LEDFNGVELYALDYFVANEFLKYLRLHVGNVNGTAGDALRFNKHYNHDLKFFTTDPKDN 363
| | | | |
Db 375 LKDWEGNEAYSLYEHFYLSSSEELNRYHLKGLTGAGKISSISQPCND----FSTKQGDN 430
| | | | |
QY 364 DRYPSNCGLYSSSGWMPDACL SANLNGKYHOKYRGVR-NGIFWGTWPGVSEAHFGGYK 422
| | | | |
Db 375 LKDWEGNEAYSLYEHFYLSSSEELNRYHLKGLTGAGKISSISQPCND----FSTKQGDN 430
| | | | |
QY 364 DRYPSNCGLYSSSGWMPDACL SANLNGKYHOKYRGVR-NGIFWGTWPGVSEAHFGGYK 422
| | | | |
Db 431 DKCIC-KCSQMLTGGWMPDAGCPNSLNGMYYPQONTNKNFGIKWYWKG-----SGY- 482
| | | | |
QY 423 SSFKEAKMIRPKGF 437
| | | | |
Db 483 -SLKATTMIRPADF 496

RESULT 10

US-09-998-833-4

; Sequence 4, Application US/09998833
; Publication No. US20030082187A1
; GENERAL INFORMATION:
; APPLICANT: THORPE, PHILIP E.
; APPLICANT: PAN, SOPHIA
; TITLE OF INVENTION: CANCER TREATMENT METHODS USING ANTIBODIES TO
; TITLE OF INVENTION: AMINOPHOSPHOLIPIDS
; FILE REFERENCE: 4001.002200
; CURRENT APPLICATION NUMBER: US/09/998,833
; CURRENT FILING DATE: 2001-11-30
; PRIOR APPLICATION NUMBER: US/09/351,543
; PRIOR FILING DATE: 1999-07-12
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 4
; LENGTH: 496
; TYPE: PRT
; ORGANISM: Homo sapiens
; ORGANISM: Homo sapiens
US-09-998-833-4

Query Match 22.0%; Score 522; DB 11; Length 496;

Best Local Similarity 27.9%; Pred. No. 1e-38;

Matches 138; Conservative 74; Mismatches 159; Indels 124; Gaps 15;

QY 43 LBSRGKCE---EAGCPYCVSLPPL-----TIQ--LPKQSRLEEVEKEYQN 84
| | | | |
Db 26 YDSIGKQYQVCHGSCSYTFLLPEMNCRSSSSPYVSNVAVQDAPLEYYDDSVQRLQVLEN 85
| | | | |
QY 85 LKE-----IVNSLKSCQCCQLQADDNCPGRNGLLPSTGAPREVGN----- 128
| | | | |
Db 86 INENNTQWLKLENYIQDNYKKEMVEIQONAVQN-----QTAVMIEIGTNLLNQ 134
| | | | |
QY 129 -----RVRELESEV-----NKLSELKNAKEEINVULHGR-----LEKL 161
| | | | |
Db 135 TABQTRKLTDEVAQVNLQTRLEQLLHLSLSTNKLKQILDQTSLEINKLQDNKSFLEKK 194
| | | | |
QY 162 N.V-----NMNNIENVVDSKVANLTP-----V 183
| | | | |
Db 195 VLAEXDKHIIQLOSTKEEKDQQLVLSKNSIIELEKKIVTATVNSVLQKQCHDLMET 254
| | | | |
QY 184 VNSLDGKSCPSQEQIQSRPVQHLYIKDCSDYYAIGKSSSETYRVTDPKNSSEFVYCD 243
| | | | |
Db 255 VNNLLTMSTNSAKDPTVAKEEQISPRDCAEVKSGHTNGIYTLTPNSTEELKAYCD 314
| | | | |
QY 244 METMGSGTVALQARDGSGTNFTTQDVKAGFGNLRREFWLGNDKIHLLTKSKEMILRID 303
| | | | |
Db 315 MEAGGGGTIIORREDGSDVDFQRTWKEVKVGFNGSGEYWLGNFVSQLTQQRVVLKIH 374
| | | | |
QY 304 LEDFNGVELYALDYFVANEFLKYLRLHVGNVNGTAGDALRFNKHYNHDLKFFTTDPKDN 363
| | | | |
Db 375 LKDWEGNEAYSLYEHFYLSSSEELNRYHLKGLTGAGKISSISQPCND----FSTKQGDN 430
| | | | |
QY 364 DRYPSNCGLYSSSGWMPDACL SANLNGKYHOKYRGVR-NGIFWGTWPGVSEAHFGGYK 422
| | | | |
Db 431 DKCIC-KCSQMLTGGWMPDAGCPNSLNGMYYPQONTNKNFGIKWYWKG-----SGY- 482
| | | | |
QY 423 SSFKEAKMIRPKGF 437
| | | | |
Db 483 -SLKATTMIRPADF 496

RESULT 1:
US-10-136-819-13
; Sequence 13, Application US/10136819
; Publication No. US20030166593A1
; GENERAL INFORMATION:
; APPLICANT: Chien, Kenneth
; APPLICANT: Hoshijima, Masahiko
; TITLE OF INVENTION: No. US20030166593A1-viral vesicle vector for cardiac specific g
; FILE REFERENCE: 6627-PAL198
; CURRENT APPLICATION NUMBER: US/10/136,819
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: 60/287,423

; PRIOR FILING DATE: 2001-04-30
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 13
; LENGTH: 496
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-136-819-13

Query Match 22.0%; Score 522; DB 12; Length 496;
Best Local Similarity 27.9%; Pred. No. le-38;
Matches 138; Conservative 74; Mismatches 159; Indels 124; Gaps 15;
QY 43 LESRGKCE---EAGECPYQVSLPPL-----TIQ--LPKQFSRIEVEVKEVQN 84
DB 26 MDSIGKKQYQVGHGSCSYTFLLPEMNCNCRSSSPYVSNVQORDAPLEYDSDVQRLQVLEN 85
QY 85 LKE-----IVNSLKSCQDCKLOADNGDPGRNGLLPSTGAPGEVGN----- 128
DB 86 IMENNTQWLKLENYIQDNMKKEWVEIQNAVQN-----QTAVMIEIGTNLLNQ 134
QY 129 -----RVRELESEV-----NKLSSSELKNKAKEEINVLRGR-----LEKJ 161
DB 135 TAEQTRKLTIDEAQLVQNLQTTRELEQLLEHSLSTNKLKQILDOOTSEINKLQDNKSFLEKK 194
QY 162 NLV-----NMNIENYVDKVNLTFF-----V 183
DB 195 VLAMEDKHIIQLOSIKEEKDQQLVNSKQNSIIIELEKK-VTATVNSVLQKQCHDLMET 254
QY 184 VNSLDGKCKCPQOEQIQSRPVQHLYKDCSDYYAIGKSSSEYRVTPDPKNSFEVYCD 243
DB 255 VNNLLTWMSTNSAKDPTVAKEEQISPRDCAEVFKSGHTTNG-YTLTFPNSTEEIKAYCD 314
QY 244 METMGSGWTVLQARLDGSTNFTTWODYKAGFGLNRREFWLGNDKIHLLTKSKEMILRID 303
DB 315 MEAGGGWTIIQRREDGSDVDFQRTWKKEYKVGFGNPSGEYWGNEFVSQLTNQGRYVLIKIH 374
QY 304 LEDFNGVELYALYDQFVAVNEFLKYLHVGNNGTAGDALRFNKNHNDLKFFTPDKDN 363
DB 375 LKDWEGNEAYSLYEHFYLSSSEELNYRIHLKGLTGITAGKISSISQPGND-----FSTKDGDN 430
QY 364 DRYPSGNGLYSSGWFDAFLSANLNGKYYHOKYRGVR-NGIFWGTWPGVSEAHPGGYK 422
DB 431 DKCIC-KCSQMLTGGWFFDAGPSNLNGYYPQRTNKFNGIKWYWKG-----SGY- 482
QY 423 SSFKEAKMIRPKHF 437
DB 483 -SLKATTMIRPADF 496

RESULT 12
US-10-179-615-6
; Sequence 6, Application US/10179615
; Publication No. US20030166857A1
; GENERAL INFORMATION:
; APPLICANT: Davis, Samuel et al.
; TITLE OF INVENTION: TIE-2 LIGANDS, METHODS OF MAKING AND USES THEREOF
; FILE REFERENCE: REG 330-F-PCT-US
; CURRENT APPLICATION NUMBER: US/10179,615
; PRIOR FILING DATE: 2002-06-24
; PRIOR FILING DATE: 2002-06-24
; PRIOR FILING DATE: 1999-09-16
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 6
; LENGTH: 496
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Unknown Organism
; US-10-179-615-6
Query Match 22.0%; Score 522; DB 12; Length 496;

Best Local Similarity 27.9%; Pred. No. le-38;
Matches 138; Conservative 74; Mismatches 159; Indels 124; Gaps 15;
QY 43 LESRGKCE---EAGECPYQVSLPPL-----TIQ--LPKQFSRIEVEVKEVQN 84
DB 26 MDSIGKKQYQVGHGSCSYTFLLPEMNCNCRSSSPYVSNVQORDAPLEYDSDVQRLQVLEN 85
QY 85 LKE-----IVNSLKSCQDCKLOADNGDPGRNGLLPSTGAPGEVGN----- 128
DB 86 IMENNTQWLKLENYIQDNMKKEWVEIQNAVQN-----QTAVMIEIGTNLLNQ 134
QY 129 -----RVRELESEV-----NKLSSSELKNKAKEEINVLRGR-----LEKJ 161
DB 135 TAEQTRKLTIDEAQLVQNLQTTRELEQLLEHSLSTNKLKQILDOOTSEINKLQDNKSFLEKK 194
QY 162 NLV-----NMNIENYVDKVNLTFF-----V 183
DB 195 VLAMEDKHIIQLOSIKEEKDQQLVNSKQNSIIIELEKK-VTATVNSVLQKQCHDLMET 254
QY 184 VNSLDGKCKCPQOEQIQSRPVQHLYKDCSDYYAIGKSSSEYRVTPDPKNSFEVYCD 243
DB 255 VNNLLTWMSTNSAKDPTVAKEEQISPRDCAEVFKSGHTTNG-YTLTFPNSTEEIKAYCD 314
QY 244 METMGSGWTVLQARLDGSTNFTTWODYKAGFGLNRREFWLGNDKIHLLTKSKEMILRID 303
DB 315 MEAGGGWTIIQRREDGSDVDFQRTWKKEYKVGFGNPSGEYWGNEFVSQLTNQGRYVLIKIH 374
QY 304 LEDFNGVELYALYDQFVAVNEFLKYLHVGNNGTAGDALRFNKNHNDLKFFTPDKDN 363
DB 375 LKDWEGNEAYSLYEHFYLSSSEELNYRIHLKGLTGITAGKISSISQPGND-----FSTKDGDN 430
QY 364 DRYPSGNGLYSSGWFDAFLSANLNGKYYHOKYRGVR-NGIFWGTWPGVSEAHPGGYK 422
DB 431 DKCIC-KCSQMLTGGWFFDAGPSNLNGYYPQRTNKFNGIKWYWKG-----SGY- 482
QY 423 SSFKEAKMIRPKHF 437
DB 483 -SLKATTMIRPADF 496

RESULT 13
US-10-179-820-6
; Sequence 6, Application US/10179920
; Publication No. US20030166858A1
; GENERAL INFORMATION:
; APPLICANT: Davis, Samuel et al.
; TITLE OF INVENTION: TIE-2 LIGANDS, METHODS OF MAKING AND USES THEREOF
; FILE REFERENCE: REG 330-F-PCT-US
; CURRENT APPLICATION NUMBER: US/10179,820
; PRIOR FILING DATE: 2002-06-24
; PRIOR FILING DATE: 2002-06-24
; PRIOR FILING DATE: 1999-09-16
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 6
; LENGTH: 496
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Unknown Organism
; US-10-179-820-6
Query Match 22.0%; Score 522; DB 12; Length 496;
Best Local Similarity 27.9%; Pred. No. le-38;
Matches 138; Conservative 74; Mismatches 159; Indels 124; Gaps 15;
QY 43 LESRGKCE---EAGECPYQVSLPPL-----TIQ--LPKQFSRIEVEVKEVQN 84
DB 26 MDSIGKKQYQVGHGSCSYTFLLPEMNCNCRSSSPYVSNVQORDAPLEYDSDVQRLQVLEN 85
QY 85 LKE-----IVNSLKSCQDCKLOADNGDPGRNGLLPSTGAPGEVGN----- 128
DB 86 IMENNTQWLKLENYIQDNMKKEWVEIQNAVQN-----QTAVMIEIGTNLLNQ 134

QY 129 -----RVRELESEV-----NKLSELKNAKEEINVLHGR---LEKL 161
DB 135 TAECTRKLTQVDAQVNLQTR-LEQLLEHSLSTNLEKQILQDQSEINKLQDKSFLK 194
QY 162 NLV-----NMNNIENYVDSKVANLTF-----V 183
DB 195 VLAMEDKHIIQLQSIKEEKQOLQVLVSKNSIIEELEKKIVTATVNSVLQKQOHLMET 254
QY 184 VNSLDGKSCKCPQOEQIQSRPVQHLIYKDCSDYYAIGKRSSETYRVTDPKNSFEVYCD 243
DB 255 VNNLLTMMSTNSAKDPTVAKEEQISFRDCAEVFKSGHTTNGIYTLTTPNS-EEIKAYCD 314
QY 244 METMGCGWTVLQARLDGSTNFTRTWODYKAGFNLRRREFWLGNDKIHLLTKSKEMILRID 303
DB 315 XEAGGGGWIIQRRDGSVDFTWKEYKVGFGNPSGEYWLGNFVSQLTNQORYVLKIH 374
QY 304 LEDFNGVELYALYDQFYVANEFLKYRLHVGNYNGTAGDALRPNKHYNHLKFTTTPKDN 363
DB 375 LKOWEGNEAYSJYEHFYLSSBELNRIHLKGLTGTAAGKISSIQPCND-----FSTKDCGN 430
QY 364 DRYPSGNCGLYSSGWMFACLSANLNGKYYHCKYRGVR-NGIFWGTWPGVSEAHFGGYK 422
DB 431 DKCIC-KCSQMLTGGWFDACGPNLNGMYFPQONTNKFNGIKVYWKG-----SGY- 482
QY 423 SSFKEAKMIRPKHF 437
DB 483 -SLKATMMIRPADF 496

RESULT 14

US-10-373-561-4
; Sequence 4, Application US/20373561
; Publication No. US20030175276A1
; GENERAL INFORMATION:
; APPLICANT: Philip E. Thorpe
; APPLICANT: Rolf A. Brekner
; TITLE OF INVENTION: ANTIBODY METHODS FOR SELECTIVELY INHIBITING VEGF
; FILE REFERENCE: 4091.002582 US/10/373,561
; CURRENT APPLICATION NUMBER: US/10/373,561
; PRIOR FILING DATE: 2003-02-24
; PRIOR APPLICATION NUMBER: US/09/561,499
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: 60/131,432
; PRIOR FILING DATE: 1999-04-28
; NUMBER OF SEQ ID NOS: 44
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
; LENGTH: 496
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-373-561-4

Query Match 22.0%; Score 522; DB 12; Length 496;
Best Local Similarity 27.9%; Pred. No. 1e-38;
Matches 138; Conservative 74; Mismatches 159; Indels 124; Gaps 15;

QY 43 LESRGKCE---EAGECPYQVSLPPL-----TIQ--LPKQFSRIEVEFKEVQN 84
DB 26 MDSIGKKQYQVHGSCSYTFLPEMNCNCRSSSPYVSNVQRDAPLEYDSDVQRLQVLEN 85
QY 85 LKE-----IVNSLKSCQCKLOADNGDPGNGLLLPSTGAPGEVGDN---- 128
DB 86 IMENNTQWLKLENYICNNMKEMVEIQNAVN-----QTAVMIEIGTNLQ 134
QY 129 -----RVRELESEV-----NKLSELKNAKEEINVLHGR---LEKL 161
DB 135 TAECTRKLTQVDAQVNLQTR-LEQLLEHSLSTNLEKQILQDQSEINKLQDKSFLK 194
QY 162 NLV-----NMNNIENYVDSKVANLTF-----V 183
DB 195 VLAMEDKHIIQLQSIKEEKQOLQVLVSKNSIIEELEKKIVTATVNSVLQKQOHLMET 254
QY 184 VNSLDGKSCKCPQOEQIQSRPVQHLIYKDCSDYYAIGKRSSETYRVTDPKNSFEVYCD 243
DB 255 VNNLLTMMSTNSAKDPTVAKEEQISFRDCAEVFKSGHTTNGIYTLTTPNS-EEIKAYCD 314
QY 244 METMGCGWTVLQARLDGSTNFTRTWODYKAGFNLRRREFWLGNDKIHLLTKSKEMILRID 303
DB 315 XEAGGGGWIIQRRDGSVDFTWKEYKVGFGNPSGEYWLGNFVSQLTNQORYVLKIH 374
QY 304 LEDFNGVELYALYDQFYVANEFLKYRLHVGNYNGTAGDALRPNKHYNHLKFTTTPKDN 363
DB 375 LKOWEGNEAYSJYEHFYLSSBELNRIHLKGLTGTAAGKISSIQPCND-----FSTKDCGN 430
QY 364 DRYPSGNCGLYSSGWMFACLSANLNGKYYHCKYRGVR-NGIFWGTWPGVSEAHFGGYK 422
DB 431 DKCIC-KCSQMLTGGWFDACGPNLNGMYFPQONTNKFNGIKVYWKG-----SGY- 482
QY 423 SSFKEAKMIRPKHF 437
DB 483 -SLKATMMIRPADF 496

QY 184 VNSLDGKSCKCPQOEQIQSRPVQHLIYKDCSDYYAIGKRSSETYRVTDPKNSFEVYCD 243
DB 255 VNNLLTMMSTNSAKDPTVAKEEQISFRDCAEVFKSGHTTNGIYTLTTPNS-EEIKAYCD 314
QY 244 METMGCGWTVLQARLDGSTNFTRTWODYKAGFNLRRREFWLGNDKIHLLTKSKEMILRID 303
DB 315 XEAGGGGWIIQRRDGSVDFTWKEYKVGFGNPSGEYWLGNFVSQLTNQORYVLKIH 374
QY 304 LEDFNGVELYALYDQFYVANEFLKYRLHVGNYNGTAGDALRPNKHYNHLKFTTTPKDN 363
DB 375 LKOWEGNEAYSJYEHFYLSSBELNRIHLKGLTGTAAGKISSIQPCND-----FSTKDCGN 430
QY 364 DRYPSGNCGLYSSGWMFACLSANLNGKYYHCKYRGVR-NGIFWGTWPGVSEAHFGGYK 422
DB 431 DKCIC-KCSQMLTGGWFDACGPNLNGMYFPQONTNKFNGIKVYWKG-----SGY- 482
QY 423 SSFKEAKMIRPKHF 437
DB 483 -SLKATMMIRPADF 496

RESULT 15
US-10-179-744-6
; Sequence 6, Application US/10179744
; Publication No. US20020173627A1
; GENERAL INFORMATION:
; APPLICANT: Davis, Samuel et al.
; TITLE OF INVENTION: TIE-2 LIGANDS, METHODS OF MAKING AND USES THEREOF
; FILE REFERENCE: REG 330-F-PCT-US
; CURRENT APPLICATION NUMBER: US/10/179,744
; CURRENT FILING DATE: 2002-06-24
; PRIOR APPLICATION NUMBER: US/08/817,318
; PRIOR FILING DATE: 1999-09-16
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 6
; LENGTH: 496
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURES:
; OTHER INFORMATION: Unknown Organism
US-10-179-744-6

Query Match 22.0%; Score 522; DB 14; Length 496;
Best Local Similarity 27.9%; Pred. No. 1e-38;
Matches 138; Conservative 74; Mismatches 159; Indels 124; Gaps 15;

QY 43 LESRGKCE---EAGECPYQVSLPPL-----TIQ--LPKQFSRIEVEFKEVQN 84
DB 26 MDSIGKKQYQVHGSCSYTFLPEMNCNCRSSSPYVSNVQRDAPLEYDSDVQRLQVLEN 85
QY 85 LKE-----IVNSLKSCQCKLOADNGDPGNGLLLPSTGAPGEVGDN---- 128
DB 86 IMENNTQWLKLENYICNNMKEMVEIQNAVN-----QTAVMIEIGTNLQ 134
QY 129 -----RVRELESEV-----NKLSELKNAKEEINVLHGR---LEKL 161
DB 135 TAEOTRKLTQVDAQVNLQTR-LEQLLEHSLSTNLEKQILQDQSEINKLQDKSFLK 194
QY 162 NLV-----NMNNIENYVDSKVANLTF-----V 183
DB 195 VLAMEDKHIIQLQSIKEEKQOLQVLVSKNSIIEELEKKIVTATVNSVLQKQOHLMET 254
QY 184 VNSLDGKSCKCPQOEQIQSRPVQHLIYKDCSDYYAIGKRSSETYRVTDPKNSFEVYCD 243
DB 255 VNNLLTMMSTNSAKDPTVAKEEQISFRDCAEVFKSGHTTNGIYTLTTPNS-EEIKAYCD 314
QY 244 METMGCGWTVLQARLDGSTNFTRTWODYKAGFNLRRREFWLGNDKIHLLTKSKEMILRID 303
DB 315 XEAGGGGWIIQRRDGSVDFTWKEYKVGFGNPSGEYWLGNFVSQLTNQORYVLKIH 374
QY 304 LEDFNGVELYALYDQFYVANEFLKYRLHVGNYNGTAGDALRPNKHYNHLKFTTTPKDN 363
DB 375 LKOWEGNEAYSJYEHFYLSSBELNRIHLKGLTGTAAGKISSIQPCND-----FSTKDCGN 430
QY 364 DRYPSGNCGLYSSGWMFACLSANLNGKYYHCKYRGVR-NGIFWGTWPGVSEAHFGGYK 422
DB 431 DKCIC-KCSQMLTGGWFDACGPNLNGMYFPQONTNKFNGIKVYWKG-----SGY- 482
QY 423 SSFKEAKMIRPKHF 437
DB 483 -SLKATMMIRPADF 496

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 5, 2003, 16:44:23 ; Search time 30.9427 Seconds
(without alignments)
600.285 Million cell updates/sec

Title: US-09-902-563-2
Perfect score: 2378
Sequence: 1 MLANWYLSAVLATYGFJ.....GYKSSFKENOMIRPQHKFP 439

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 328717 seqs, 42310858 residues

Total number of hits satisfying chosen parameters: 328717

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA:
1: /cgn2_6/prodata/1/iaa/5A_COVR pep.*
2: /cgn2_6/prodata/1/iaa/5B_COVR pep.*
3: /cgn2_6/prodata/1/iaa/6A_COVR pep.*
4: /cgn2_6/prodata/1/iaa/6B_COVR pep.*
5: /cgn2_6/prodata/1/iaa/PCFUS_COM3 pep.*
6: /cgn2_6/prodata/1/iaa/backfiles1 pep.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2375	100.0	439	4	US-09-442-143A-2
2	1853.5	77.9	432	4	US-09-442-143A-4
3	524	22.0	314	1	US-08-525-505A-2
4	524	22.0	496	4	US-09-302-491-7
5	522	22.0	483	3	US-08-740-223A-8
6	522	22.0	480	4	US-09-709-188-6
7	522	22.0	496	1	US-08-373-579-6
8	522	22.0	496	2	US-08-418-595-6
9	522	22.0	496	2	US-08-665-926-6
10	522	22.0	496	3	US-09-562-437-6
11	522	22.0	496	3	US-08-740-223A-6
12	522	22.0	496	4	US-09-351-457-4
13	522	22.0	496	4	US-09-561-500-4
14	522	22.0	496	4	US-09-561-108-4
15	522	22.0	496	4	US-09-351-543-4
16	522	22.0	496	4	US-09-561-526-4
17	522	22.0	496	4	US-09-202-491-8
18	522	22.0	496	4	US-08-817-318-6
19	522	22.0	496	4	US-09-709-188-6
20	522	22.0	496	4	US-09-561-499-4
21	521.5	21.9	498	3	US-08-740-223A-20
22	521.5	21.8	499	3	US-08-740-223A-24
23	517.5	21.8	499	4	US-09-709-188-24
24	510	21.4	496	3	US-09-740-223A-15
25	510	21.4	496	4	US-09-709-188-15
26	510	21.4	496	4	US-09-960-507-20
27	506.5	21.3	286	3	US-08-960-507-20

28 506.5 21.3 286 4 US-09-136-801-20 Sequence 20, Appl
29 506.5 21.3 286 4 US-09-202-088A-20 Sequence 20, Appl
30 506 21.3 312 1 US-08-525-505A-4 Sequence 4, Appl
31 505 21.2 491 2 US-08-933-821-4 Sequence 4, Appl
32 505 21.2 491 3 US-08-960-507-4 Sequence 4, Appl
33 505 21.2 491 4 US-09-136-828-4 Sequence 4, Appl
34 505 21.2 491 4 US-09-332-928A-4 Sequence 4, Appl
35 505 21.2 491 4 US-09-136-801-4 Sequence 4, Appl
36 505 21.2 491 4 US-09-332-929-4 Sequence 4, Appl
37 505 21.2 491 4 US-09-333-075-4 Sequence 4, Appl
38 505 21.2 491 4 US-09-202-088A-4 Sequence 4, Appl
39 505 21.2 491 4 US-09-333-077-4 Sequence 4, Appl
40 500 21.0 491 4 US-09-658-544-2 Sequence 2, Appl
41 498 20.9 496 3 US-08-740-223A-16 Sequence 16, Appl
42 498 20.9 496 4 US-09-709-188-16 Sequence 16, Appl
43 489 20.6 346 3 US-08-960-507-19 Sequence 19, Appl
44 489 20.6 346 4 US-09-136-801-19 Sequence 19, Appl
45 489 20.6 346 4 US-09-202-088A-19 Sequence 19, Appl

ALIGNMENTS

RESULT 1
US-09-442-143A-2
; Sequence 2, Application US/09442143A
; Patent No. 6403089
; GENERAL INFORMATION:
; APPLICANT: Levy, Gary
; APPLICANT: Clavik, David A.
; TITLE OF INVENTION: Methods of Modulating Immune Coagulation;
; FILE REFERENCE: 9579-14
; CURRENT APPLICATION NUMBER: US/09442143A
; PRIOR FILING DATE: 1999-11-15
; PRIOR APPLICATION NUMBER: US 60/346,537
; PRIOR FILING DATE: 1997-05-17
; PRIOR APPLICATION NUMBER: US 60/361,684
; PRIOR FILING DATE: 1997-10-10
; NUMBER OF SEQ ID NOS: 53
; SOFTWARE: Patent version 3.1
; SEQ ID NO 2
; LENGTH: 439
; TYPE: PRT
; ORGANISM: Homo sapiens fgl2
US-09-442-143A-2

Query Match:	100.0%;	Score 2378;	DB 4;	Length 439;
Best Local Similarity:	100.0%;	Pred. No. 8e-211;		
Matches 439;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
QY	1	MLANWYLSAVLATYGF	LVVANNTEETIKDERAKDVCPVRL	ESRGKCEAGECPYQVS 60
DB	1	MLANWYLSAVLATYGF	LVVANNTEETIKDERAKDVCPVRL	ESRGKCEAGECPYQVS 60
QY	61	LPPLTIQLPKQFSRIE	EVFKEVQNLKEIVNSLKSCDCKLQ	ADNDGDPGRNGLLLPSTG 120
DB	61	LPPLTIQLPKQFSRIE	EVFKEVQNLKEIVNSLKSCDCKLQ	ADNDGDPGRNGLLLPSTG 120
QY	121	APGEVGNRVRELESEVNKLSSELNAKEE	ETNVLHGRLKLNIVNMNNIENYVDSKVANL 180	
DB	121	APGEVGNRVRELESEVNKLSSELNAKEE	ETNVLHGRLKLNIVNMNNIENYVDSKVANL 180	
QY	181	TFVNSLDGKSKCPSEQIQSRPVOHLLYK	DCSDYAIKGRSETYRVTPDPKNSSEFV 240	
DB	181	TFVNSLDGKSKCPSEQIQSRPVOHLLYK	DCSDYAIKGRSETYRVTPDPKNSSEFV 240	
QY	241	YCDMETMGGMVTVQARLDGSGTNFT	RTWQYKAGFGNLRREFWLNKDHIHLLTKSKEMIL 300	
DB	241	YCDMETMGGMVTVQARLDGSGTNFT	RTWQYKAGFGNLRREFWLNKDHIHLLTKSKEMIL 300	
QY	301	RIDLEDNGVELYALYDQFYVANEFLKY	RLHVGNYNGTAGDALARFNKHYNHDKFFFTPD 360	
DB	301	RIDLEDNGVELYALYDQFYVANEFLKY	RLHVGNYNGTAGDALARFNKHYNHDKFFFTPD 360	


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CY 361 KNDYPSGNCGLYYSGWFWFACLSANLNGKYHCKYGVNRNGIFWGTWPGVSEAHPPGG 420
DB 361 KNDYPSGNCGLYYSGWFWFACLSANLNGKYHCKYGVNRNGIFWGTWPGVSEAHPPGG 420
CY 421 YKSFKEAKMIRPKFKP 439
DB 421 YKSFKEAKMIRPKFKP 439

RESULT 2
US-09-442-143A-4
; Sequence 4, Application US/09442143A
; Patent No. 6403089
; GENERAL INFORMATION:
; APPLICANT: Levy, Gary
; APPLICANT: Clark, David A.
; TITLE OF INVENTION: Methods of Modulating Immune Coagulation
; FILE REFERENCE: 9579-14
; CURRENT APPLICATION NUMBER: US/09/442,143A
; PRIOR FILING DATE: 1999-11-15
; PRIOR APPLICATION NUMBER: US 60/046,537
; PRIOR FILING DATE: 1997-05-17
; PRIOR APPLICATION NUMBER: US 60/051,684
; PRIOR FILING DATE: 1997-10-10
; NUMBER OF SEQ ID NOS: 53
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 4
; LENGTH: 432
; TYPE: PRT
; ORGANISM: Murine fg-2
US-09-442-143A-4
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Query Match 77.9%; Score 1853.5; DB 4; Length 432;
Best Local Similarity 77.7%; Pred. No. 1.7e-162;
Matches 341; Conservative 42; Mismatches 49; Indels 7; Gaps 4;
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CY 1 MKLANWYLSAVLATYGVFLVANNETEEIKDERAKDVCVRLESRGKCBEEAGECYQWS 60
DB 1 MRLPGWLLSSAVLAACR-AVEEHNLTGLEDASAAQAPARLEGSGRC-EGSQCPFLT 59
CY 61 LPPLTICLPQFSRIEVEFVEQNEKEIVNSLKKSCODCKLQADDNGDGRNGLLPSTG 120
DB 59 LPPLTICLPQJGSMEEVLEKVRTEKAVDSLKKSCQCKLQACDHRDPGNG-NGG 114
CY 121 APGEVGNRVRELESEVNVKLSSELKNAKEEINVHLHSEJEKLNLYNMNNENYVDSKVANL 180
DB 115 AE-TAEDSRVCELESQVNLKSELKNAKDQIQGLQGRLETLHLVNMNNENYVDENKVANL 173
CY 181 TFVNSLDGKCKSCPSQEQIOSRVOHLIYKDCSDYVAIGKRSSETYRVTPDPKNSFEV 240
DB 174 TVVNSLDGKCKSCPSQEQHMQSQVQHLIYKDCSDYVJGRRSSGATRVTPDRNSSFV 233
CY 241 YCDMETVGGGTVLQARLDGSTNFTRTWQDYKAGFNLRRREFWLGNDKIHLLTKSEVIL 300
DB 234 YCDMETVGGGTVLQARLDGSTNFTREWKDYKAGFNLRRREFWLGNDKIHLLTKSEVIL 293
CY 301 RIDUEDFNGVELYALYQFYVANEFLYRLHVGNYNGTAGALAFNKGKHYHDKFFTPD 360
DB 294 RIDUEDFNGULTYALYQFYVANEFLYRLHVGNYNGTAGALAFNKGKHYHDLRFFTPD 353
CY 361 KNDYPSGNCGLYYSGWFWFACLSANLNGKYHCKYGVNRNGIFWGTWPGVSEAHPPGG 420
DB 354 RNDYPSGNCGLYYSGWFWFDCLSANLNGKYHCKYGVNRNGIFWGTWPGVSEAHPPGG 413
CY 421 YKSFKEAKMIRPKFKP 439
DB 414 YKSFKEAKMIRPKFKP 432
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RESULT 3
US-08-525-505A-2
; Sequence 2, Application US/08525505A
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; Patent No. 5867711
; GENERAL INFORMATION:
; APPLICANT: HARA, HIROSHI
; APPLICANT: YOSHIMURA, HIROMITSU
; APPLICANT: SATSUKI, YUMIKO
; APPLICANT: SHINDO, SAKKO
; APPLICANT: HANAJA, KAZUNORI
; TITLE OF INVENTION: PARENCHYMAL HEPTOCYTE GROWTH SUBSTANCE
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
; STREET: 1255 S. JEFFERSON DAVIS HIGHWAY, SUITE 400
; CITY: ARLINGTON
; STATE: VA
; COUNTRY: USA
; ZIP: 22202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/525,505A
; FILING DATE: 22-SEP-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/JP94/00455
; FILING DATE: 22-MAR-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 05-063905
; FILING DATE: 23-MAR-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: OBLON, NORMAN F.
; REGISTRATION NUMBER: 24,618
; REFERENCE/DOCKET NUMBER: 4587-012-0 PCT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-413-3000
; TELEFAX: 703-413-2220
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 314 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-525-505A-2

Query Match 22.0%; Score 524; DB 1; Length 314;
Best Local Similarity 37.6%; Pred. No. 3.9e-40;
Matches 124; Conservative 46; Mismatches 104; Indels 56; Gaps 13;

CY 125 VCD-NRVRE---LESEVNVKLSSELKNAKEEINVHLHSEJEKLNLYNMNNENYVDSKVAN 179
DB 23 LGDENCLQECVRLRAQVRQLETRVRKQCVVIAQLLHEK--EVQFLDRQEQDSFID----- 75
CY 180 LTFVNSLDGKCKSCPSQEQIOSRVOHLIYKDCSDYVAIGKRSSETYRVTPDPKNSSFE 239
DB 76 -----LGGK-----RH--YADCSEIYNDGFGHSGFYKIKPQLQSLABFS 111
CY 240 YCDMETVGGGTVLQARLDGSTNFTRTWQDYKAGFNLRRREFWLGNDKIHLLTKSK 296
DB 112 VYCDMSD-GGGTVLQRRSDGSENFNRQNDYENGFGNFGVOSNGEYWGKNKINILTYQG 170
CY 297 EMILRIDEDFNGVELYALYQFYVANEFLYRLHVGNYNGTAGALAFNKGKHYHDKFFTPD 350
DB 171 DVTLKIDLTDFEKNRFACYEKFVDEKSFYELNIGEYSGTAGDSLSTGTFHPEVQWNAS 230
CY 351 HDLKEFTTDFKNDYPSGNCGLYYSGWFWFACLSANLNGKYHCKYGVNRNGIFWGTWPG 409
DB 231 HOTMKFSTRDRONDY-NGNCAEEQSGMWFNRCHSANLNGVYQGPYRAETDNGWVYT 289
CY 410 WPGVSEAHPPGGYKSFKEAKMIRPKFKP 439
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Db 290 W-----RGWYSLKSVVMKIRPSDFIE 311

RESULT 4

US-09-202-491-7
; Sequence 7, Application: US/09202491
; Patent No. 6432667
; GENERAL INFORMATION:
; APPLICANT: Valenzuela et al.
; TITLE OF INVENTION: NOVEL LIGANDS, METHODS OF MAKING AND USES THEREOF
; FILE REFERENCE: REG330-K
; CURRENT APPLICATION NUMBER: US/09/202,491
; CURRENT FILING DATE: 1998-11-16
; EARLIER APPLICATION NUMBER: PCT/US97/10728
; EARLIER FILING DATE: 1997-06-19
; EARLIER APPLICATION NUMBER: 60/022,999
; EARLIER FILING DATE: 1996-08-02
; EARLIER APPLICATION NUMBER: 60/021,087
; EARLIER FILING DATE: 1996-07-02
; EARLIER APPLICATION NUMBER: 08/665,926
; EARLIER FILING DATE: 1996-06-19
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 7
; LENGTH: 496
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-202-491-7

Query Match 22.0%; Score 524; DB 4; Length 496;
Best Local Similarity 32.9%; Pred. No. 7.8e-40;
Matches 127; Conservative 65; Mismatches 154; Indels 40; Gaps 9;
QY 61 LPPLTIQLPKQFRIEVEPVKQMLKEIVNSLKKSCQCKLQADNGCPGNSLALPSTG 120
Db 142 LTDVEAQVLTQTL-----ELQLGHSISTNKLKQLDQTSINKLNKNSFL----- 191
QY 121 APGEVGNRVRELESEVKNLSLKNKKEEIVNLHGR-----EKLKLVMMNRIKY 172
Db 192 -----ECKVLDEGKHSQQLQSKQCKQELQVLVSKQSSVIDEKLKLVATVNN--SJ 243
QY 173 VDSKVANLTVNSLQCKKSCQPSQEQIOSRPVQHJYKDCSYVAIGKSSSTYRPTD 232
Db 244 LKQCHQDMEVNSLTLTWASPSNKSVAIRKEQTTFRCAIFKSLTTSIYTLTP 303
QY 233 PKSSFEVYCDMTGGTGVQLQARLDGSTNFTRTQDYKAGFGNLRREFWZGNKIHLL 292
Db 304 NSTEEIKAYCDVGGGGVVIQHREDGSDVDFQRTWKYKEGFGNPLGEVWLGNEFVSQ 363
QY 293 TKSKEMLRLDLEDFNGVELYALDQFYVANEFKYLRLHVGNYNGTAGDALRKNKHND 352
Db 364 TGQHRVYVKIQKDWEGNEAHSYDHFYLAGESNRYHLTGJGTAAKISS-SQPSD- 422
QY 353 LKFFPTPDNDPVPNSGCLGYSSGWWFADCLSANLNGKYHCKYRGVR-NGIPWGTNP 411
Db 423 ---FSTKSDNDKIC-C-KCSQMLSGGWWFADCGPSNLNGQYIFCKQNTNKGINKYWK 478
QY 412 GVSEAHPGYKSSFKKAXMYRPHF 437
Db 479 G-----SGY--SLKATTNMRPADE 496

RESULT 5

US-08-740-223A-8
; Sequence 8, Application US/08740223A
; Patent No. 6265564
; GENERAL INFORMATION:
; APPLICANT: Davis, et al.
; TITLE OF INVENTION: Expressed Ligand - Vascular
; TITLE OF INVENTION: Inter cellular Signalling Molecule
; NUMBER OF SEQUENCES: 28
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Regeneron Pharmaceuticals, Inc.

STREET: 777 Old Saw Mill Road
City: Tarrytown
STATE: NY
COUNTRY: USA
ZIP: 10591
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/740,223A
FILING DATE: 25-OCT-1996
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 60/022/999
FILING DATE: 02-AUG-1996
ATTORNEY/AGENT INFORMATION:
NAME: Cobert, Robert J
REGISTRATION NUMBER: 36,108
REFERENCE/DOCKET NUMBER: REG 333
TELECOMMUNICATION INFORMATION:
TELEPHONE: 914-345-7400
TELEFAX: 914-345-7721
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 480 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
FEATURE:
NAME/KEY: Mature TL2 protein
LOCATION: 1...480
OTHER INFORMATION:
US-08-740-223A-8

Query Match 22.0%; Score 522; DB 3; Length 480;
Best Local Similarity 27.9%; Pred. No. 1.1e-39;
Matches 138; Conservative 74; Mismatches 159; Indels 124; Gaps 15;
QY 43 LESRKCE---EAGBCPYQVSLPPL-----TIQ--LPKQPSRIEEVPEYQN 84
Db 10 MDSICKKYQYQHGSCSYTFLPKMDCRSCSSPVVNAVODAPLEYDDSVORLOVLEN 69
QY 85 LKE-----IVNSLKKSCQCKLQADNGCPGNGLLLPSTGAPSEVGN----- 128
Db 70 IMENNTQMLKLENYIQNMKKEMVEIQCNAYQN-----QTAVMIEIGTNLLNQ 118
QY 129 -----RVRELESEV-----NKLSSLEKNKKEEIVNLHGR---LEKL 161
Db 119 TAEQTRKLTDEAQLVNOTTRELQJLLEHSLSTNKLKQLDQTSINKLQCKNSFLEKK 178
QY 162 NLV-----NMNNIENVYDVKVANLTP-----V 183
Db 179 VLAMEDKHILQLOSIKEEKQQLQVLVSKQNSI--BELEKKIVTAVNSVLQKQCHLME 238
QY 184 VNSLDGKCKSPSQEQIOSRPVQHLYKDCSDYVAIGKRSSETYRVTDPKNSSEFVCD 243
Db 239 VNNLLTMNSTNSAKDPTVAKEEQISFRDCAEVKSGHTTNGIYTLTPNSTEEIKAYCD 298
QY 244 METMGGHTVLOARLDGSTNFTRTQDYKAGFGNLRREFWZGNKIHLLTKSKEMILRID 303
Db 299 MEAGGGGWTIIQRREDGSDVDFQRTWKYKVGFGNPSGYWLGNEFVSQJTCQRYVLKIH 358
QY 304 LEDFNGVELYALDQFYVANEFKYLRLHVGNYNGTAGDALRKNKHNDLKFFPTPDND 363
Db 359 LKDWEGNEAYSLEYEHFYLSSSEELNRYHLKGLTGAGKISSISQPGND----FSTKGD 414
QY 364 DRYPSGNCGLYSSGWWFADCLSANLNGKYHCKYRGVR-NGIPWGTNPVGVSEAHPGYK 422
Db 415 DKCIC-KCSQMLTGGWFWFADCGPSNLNGMYYPQRTNKNKNGIKMYWK-----SGY- 466

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QY 423 SSFKEAKGQIRPKHF 437
Db 467 -SLKATTMIRPADF 480

RESULT 6
US-09-709-188-8
; Sequence 8, Application US/09709188
; Patent No. 644137
; GENERAL INFORMATION:
; APPLICANT: Davis et al.
; TITLE OF INVENTION: Expressed Ligand - Vascular Inter cellular Signaling Molecule
; FILE REFERENCE: REG 333-2
; CURRENT APPLICATION NUMBER: US/09/709,188
; PRIOR FILING DATE: 2000-11-09
; PRIOR APPLICATION NUMBER: 08/740,223
; PRIOR FILING DATE: 1996-10-25
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 8
; LENGTH: 480
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-709-188-8

Query Match 22.0%; Score 522; DB 4; Length 480;
Best Local Similarity 27.9%; Pred. No. 1.1e-39;
Matches 138; Conservative 74; Mismatches 159; Indels 124; Gaps 15;

QY 43 LESRGKCE--EAGECPYQVSLPPL-----TIQ--LPKQFSRIEEVFKEVQN 84
Db 10 MDSIGKKQYQVGHGSCSYTFLPENCRCRSSSPYVSNVAVORDAPLEYDSDSVORLQVLEN 69
QY 85 LKE-----IVNSLKKSCQCKLQADDNGDPGRNGLLLPSTGAPGEVGN--- 128
Db 70 IMENNTQWLKMLKLENYIQDNMKEMVEIQONAVQN-----QAVMIEIGTNLNLQ 118
QY 129 -----RVRELESEV-----NKLSELKNAAKEEINVJHGR---LEK 161
Db 119 TAEQTRKLTQVEAQVNLQTTRELEQLLEHSLSTNKLKQLDQTSSEINKLQDNKSFLEKK 178
QY 162 NLV-----NMNNIENYVDSKVANLTF-----V 183
Db 179 VLAMEDKHIIQLQSIKEKCDQLQVLVSKNSIIEEKKIVTATVNNSVLQKQCHLMET 234
QY 184 VNSLDGKSKCPSQEQIQSRPVCHELKYKCDSDYVAIGKRSSEYRVTPDPKNSSFVYCD 243
Db 239 VNNLTMMSTNSAKDPTVAKEEQISFRDCAEVFKSGHTTNGVYTLTFPNSTEEIKAYCD 284
QY 244 METMGSGTWVLAARDLGGSTNFTRTWQDYKAGFGNLRREFNLGNDKIHLLTKSKEMILRID 303
Db 299 MEAGGGGTIIQRRDGGSDVDFORTWKEYKVGFGNPSGEYNLGNFEVFSQLTNQORYVVKIH 358
QY 304 LEDPNGVELYALYQCFYVANEFLAYRVLHVGNYNGTAGDALRPNKHYNHDLKFTTTPKON 363
Db 359 LKDWEGREAVSLYEHFYLSSLELYRHLKGLTGACKISISQPGND-----ESTKQSDN 414
QY 364 DRYPSNGCLYYSGGWFFDACSNLNGKYYHQYKRGVR-NGIPWGTPWGVSHPGSGYK 422
Db 415 DKCIC-KCSQMLTGGWFFDACGPNLNGMYVYQPCNTNKGINKMYWKG-----SGY- 466
QY 423 SSFKEAKGQIRPKHF 437
Db 467 -SLKATTMIRPADF 480

RESULT 7
US-08-373-579-6
; Sequence 6, Application US/08373579
; Patent No. 5650490
; GENERAL INFORMATION:
; APPLICANT: Davis, et al.
; TITLE OF INVENTION: TIE-2 LIGAND, METHOD OF MAKING AND USES
```

```
;
;
; TITLE OF INVENTION: THEREOF
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Regeneron Pharmaceuticals, Inc.
; STREET: 777 Old Saw Mill River Road
; CITY: Tarrytown
; STATE: New York
; COUNTRY: USA
; ZIP: 10591
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.33
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/373,579
; FILING DATE: 17-JAN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/353,503
; FILING DATE: 09-DEC-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/348,492
; FILING DATE: 02-DEC-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/330,261
; FILING DATE: 27-OCT-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/319,932
; FILING DATE: 07-OCT-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Cobert, Robert C.
; REGISTRATION NUMBER: 36,108
; REFERENCE/DOCKET NUMBER: REG 330-D
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (914) 345-7400
; TELEFAX: (914) 345-7721
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 496 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; VCLESCULE TYPE: protein
US-08-373-579-6
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Query Match 22.0%; Score 522; DB 1; Length 496;
Best Local Similarity 27.9%; Pred. No. 1.2e-39;
Matches 138; Conservative 74; Mismatches 159; Indels 124; Gaps 15;

QY 43 LESRGKCE---EAGECPYQVSLPPL-----TIQ--LPKQFSRIEEVFKEVQN 84
Db 26 MDSIGKKQYQVGHGSCSYTFLPENCRCRSSSPYVSNVAVORDAPLEYDSDSVORLQVLEN 85
QY 65 LKE-----IVNSLKKSCQCKLQADDNGDPGRNGLLLPSTGAPGEVGN--- 128
Db 86 IMENNTQWLKMLKLENYIQDNMKEMVEIQONAVQN-----QAVMIEIGTNLNLQ 134
QY 129 -----RVRELESEV-----NKLSELKNAAKEEINVJHGR---JSLK 161
Db 135 TAEQTRKLTQVEAQVNLQTTRELEQLLEHSLSTNKLKQLDQTSSEINKLQDNKSFLEKK 194
QY 162 NLV-----NMNNIENYVDSKVANLTF-----V 183
Db 195 VLAMEDKHIIQLQSIKEKCDQLQVLVSKNSIIEEKKIVTATVNNSVLQKQCHLMET 254
QY 184 VNSLDGKSKCPSQEQIQSRPVCHELKYKCDSDYVAIGKRSSEYRVTPDPKNSSFVYCD 243
Db 255 VNNLTMMSTNSAKDPTVAKEEQISFRDCAEVFKSGHTTNGVYTLTFPNSTEEIKAYCD 314
QY 244 METMGSGTWVLAARDLGGSTNFTRTWQDYKAGFGNLRREFNLGNDKIHLLTKSKEMILRID 303
Db 315 MEAGGGGTIIQRRDGGSDVDFORTWKEYKVGFGNPSGEYNLGNFEVFSQLTNQORYVVKIH 374
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US-09-665-926-6

Query Match 22.0%; Score 522; DB 2; Length 496;
Best Local Similarity 27.9%; Pred. No. 1.2e-39;
Matches 138; Conservative 74; Mismatches 159; Indels 124; Gaps 15;

QY 43 LESRGKCE--EAGECPYQVSLPPL-----TIQ--LPKQPSRIEEVKEVQN 84
DB 26 MDSIGKKQYQVCHGSCSYTFLLPEMNCRRSSSPYVNAVQDAPLEYDSVQVLQVLEN 85
QY 85 LKE-----IVNSLKKSCQCKLQADNDGPRNGLLLPSTGAFGEVGN----- 128
DB 86 IMENNTQWLKLENYIDNKXEMVEIQQNAVQN-----QTAVVIEIGTNLLNQ 134
QY 129 -----RVRELESEV-----NKLSELKNAKEEINVHGR-----LEKL 161
DB 135 TAEQTRKLTQVQVNLQTTTLEQLLEHSLSTNKLKQILDOTSEINKLQCKNSFLEKK 194
QY 162 NLV-----NMNNIENVYDLSKVANLTF-----V 183
DB 195 VLAMEDKHIIQOSIKKEKQDLQVLVSKQNSIIELEKKIVITATVNSVLOKQCHDLMET 254
QY 184 VNSLGGKCKPCSQEQIQRFPVQHLIYKQCSYVAIGKRSSETYRVTPQPKSSFEVYCD 243
DB 255 VNLLTMVSTNSAKDPTVAKEEQISFRDCAEVFKSGHTINGYTLTPPNSTEEEKAYCD 314
QY 244 METWGGGWTVLQARLDGSTNFTTWQCYKAGFGLNLRREFWLGNDKIHLLTKSEVILRID 303
DB 315 MEAGGGGWTTIQRREDSDVDFTWKEYKVGFGNPSGEYWLGNFEVSQLTNQCYVULKH 374
QY 304 LEDFNGVELYALDYQFYVANEFLKYLHVGNVNGTAGDALRFRKNHYNHDLKFFTPDKDN 363
DB 375 LKDWEGNEAYSLYEHFYLSEELNYRIHLKGLTGATKSSISQPGND-----FSTKQGN 430
QY 364 DRYPSGNCGLYSSGWWFPADECLSANLNGKYHQYKRGVR-NGFWGTWPGVSEAHPGGYK 422
DB 431 DKCIC-KCSQMLTGGWFWFACGSPNLNGMYYPQQRNTNKFNG:KYYKKG-----SGY- 482
QY 423 SSFKEAKMIRPKHF 437
DB 483 -SLKATTMIRPADF 496

RESULT 10

US-09-162-437-6
; Sequence 6, Application US/09162437
; Patent No. 6165185
; GENERAL INFORMATION:
; APPLICANT: Davis, et al.
; TITLE OF INVENTION: TIE-2 LIGAND, METHOD OF MAKING AND USES
; TITLE OF INVENTION: THEREOF
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Regeneron Pharmaceuticals, Inc.
; STREET: 777 Old Saw Mill River Road
; CITY: Tarrytown
; STATE: New York
; COUNTRY: USA
; ZIP: 10591
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/162.437
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/418,595
; FILING DATE: 06-APR-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/373,579

RESULT 11

US-08-740-223A-6
; Sequence 6, Application US/08740223A
; Patent No. 6265564
; GENERAL INFORMATION:

FILING DATE: 17-JAN-1995
APPLICATION NUMBER: US 08/353,503
FILING DATE: 09-DEC-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/348,492
FILING DATE: 02-DEC-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/330,261
FILING DATE: 27-OCT-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/319,932
FILING DATE: 07-OCT-1994
ATTORNEY/AGENT INFORMATION:
NAME: Covert, Robert J.
REGISTRATION NUMBER: 36,108
REFERENCE/DOCKET NUMBER: REG 330-D
TELECOMMUNICATION INFORMATION:
TELEPHONE: (914) 345-7400
TELEFAX: (914) 345-7721
INFORMATION FOR SEQ ID NO. 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 496 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-162-437-6

Query Match 22.0%; Score 522; DB 3; Length 496;
Best Local Similarity 27.9%; Pred. No. 1.2e-39;
Matches 138; Conservative 74; Mismatches 159; Indels 124; Gaps 15;

QY 43 LESRGKCE--EAGECPYQVSLPPL-----TIQ--LPKQPSRIEEVKEVQN 84
DB 26 MDSIGKKQYQVCHGSCSYTFLLPEMNCRRSSSPYVNAVQDAPLEYDSVQVLQVLEN 85
QY 85 LKE-----IVNSLKKSCQCKLQADNDGPRNGLLLPSTGAFGEVGN----- 128
DB 86 IMENNTQWLKLENYIDNKXEMVEIQQNAVQN-----QTAVVIEIGTNLLNQ 134
QY 129 -----RVRELESEV-----NKLSELKNAKEEINVHGR-----LEKL 161
DB 135 TAEQTRKLTQVQVNLQTTTLEQLLEHSLSTNKLKQILDOTSEINKLQCKNSFLEKK 194
QY 162 NLV-----NMNNIENVYDLSKVANLTF-----V 183
DB 195 VLAMEDKHIIQOSIKKEKQDLQVLVSKQNSIIELEKKIVITATVNSVLOKQCHDLMET 254
QY 184 VNSLGGKCKPCSQEQIQRFPVQHLIYKQCSYVAIGKRSSETYRVTPQPKSSFEVYCD 243
DB 255 VNLLTMVSTNSAKDPTVAKEEQISFRDCAEVFKSGHTINGYTLTPPNSTEEEKAYCD 314
QY 244 METWGGGWTVLQARLDGSTNFTTWQCYKAGFGLNLRREFWLGNDKIHLLTKSEVILRID 303
DB 315 MEAGGGGWTTIQRREDSDVDFTWKEYKVGFGNPSGEYWLGNFEVSQLTNQCYVULKH 374
QY 304 LEDFNGVELYALDYQFYVANEFLKYLHVGNVNGTAGDALRFRKNHYNHDLKFFTPDKDN 363
DB 375 LKDWEGNEAYSLYEHFYLSEELNYRIHLKGLTGATKSSISQPGND-----FSTKQGN 430
QY 364 DRYPSGNCGLYSSGWWFPADECLSANLNGKYHQYKRGVR-NGFWGTWPGVSEAHPGGYK 422
DB 431 DKCIC-KCSQMLTGGWFWFACGSPNLNGMYYPQQRNTNKFNGIKWYKKG-----SGY- 482
QY 423 SSFKEAKMIRPKHF 437
DB 483 -SLKATTMIRPADF 496


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RESULT 13
US-09-561-500-4
; Sequence 4, Application US/09561:500
; Patent No. 6342219
; GENERAL INFORMATION:
; APPLICANT: Philip E. Thorpe
; APPLICANT: Rolf A. Brekken
; TITLE OF INVENTION: ANTIBODY COMPOSITIONS FOR SELECTIVELY INHIBITING VEGF
; FILE REFERENCE: 4001.002500
; CURRENT APPLICATION NUMBER: US/09/561,500
; CURRENT FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: 60/131,432
; PRIOR FILING DATE: 1999-04-28
; NUMBER OF SEQ ID NOS: 44
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
; LENGTH: 496
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-561-500-4

Query Match      22.0%; Score 522; DB 4; Length 496;
Best Local Similarity 27.9%; Pred. No. 1.2e-39;
Matches 138; Conservative 74; Mismatches 159; Indels 124; Gaps 15;

QY 43 LESRGKCE---EAGECPYQVSLPPL-----TIQ--LPKQFSRIEEVKEVQN 84
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
D5 26 MDSIGKQVQVHGSCSY*FLLPENDCRSSSSPVVSNVAVORDAPLEYDVSQVORLQVLE 85
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 85 LKE-----IVNLSKSCQCKQADNDGPGRNGLLLPSTGAPGEVCN----- 128
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
D5 86 IMENNTQWLKLENYIQDNMKKEMVEIQNAVQN-----QTAVMIEIGTNLLNQ 134
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 129 -----RVRELESEV-----NKLSELKNAKEE--NVLHGR---LEKL 161
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
D5 135 TAEOTRKLTDVEAQLNQT*RLLEQLLEHSLSTNKLKQILDQTSINKLQDKNSFLEKK 194
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 162 NLV-----NMNNIENYVDKSVANLTF-----V 183
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
D5 195 VLAMEDKHIIQLQS:KEEKDQLVLVSKQNSI:EELEKKIVTATVNSVLQKQOHDLMET 254
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 184 VNSLDGKSCKPSQEQIQSRPVQHLYKDCSDYYAIGKRSSEYRVTPDPKNSSEFYVCD 243
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
D5 255 VNNLLTWMTSNAKPTVAKEQISFRDCAEVFKSGHTNGIYTLTFNTEBIAKAYCD 314
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 244 METMGGGWTVLQARLDGSTNFTRTWQDYKAGFNLRRREFWLGNDKIHLLTKSKEMILRID 303
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
D5 315 MEAGGGWTIIQRREDGSDVDFORTWKEYKVGFGNPSGEYWLGNFVSLTNQORYVLKIH 374
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 304 LEDFNGVELYALYQFYVANEFLKYRLHVGNYNGTAGDALRFNKHYNHDLKFFTPDKDN 363
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
D5 375 LKDWEGNEAVSLYEHFVLSSEELNRYIHLKGLTGTAGKISSISQPGND----FSTKQDGN 430
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 364 DRYPSGNCGLYSSGWMFQACLSANLNGKYHOKYGVGR--NGIFMGWPGVSEAHPSGYK 422
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
D5 431 DKCIC-KCSQMLTGGWAFDAGPSNLNGYYPQONTNKFNGIKYIWKG-----SGY- 482
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 423 SSFKEAKNMIRPKHF 437
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
D5 483 -SLKATTMMIRPADF 496
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

RESULT 14
US-09-561-108-4
; Sequence 4, Application US/09561:108
; Patent No. 6342221
; GENERAL INFORMATION:
; APPLICANT: Philip E. Thorpe
; APPLICANT: Rolf A. Brekken
; TITLE OF INVENTION: ANTIBODY CONJUGATE COMPOSITIONS FOR SELECTIVELY INHIBITING VEGF
; FILE REFERENCE: 4001.002584
; CURRENT APPLICATION NUMBER: US/09/561,108
```

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; CURRENT FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: 60/131,432
; PRIOR FILING DATE: 1999-04-28
; NUMBER OF SEQ ID NOS: 44
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
; LENGTH: 496
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-561-108-4

Query Match      22.0%; Score 522; DB 4; Length 496;
Best Local Similarity 27.9%; Pred. No. 1.2e-39;
Matches 138; Conservative 74; Mismatches 159; Indels 124; Gaps 15;

QY 43 LESRGKCE---EAGECPYQVSLPPL-----TIQ--LPKQFSRIEEVKEVQN 84
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
D5 26 MDSIGKQVQVHGSCSY*FLLPENDCRSSSSPVVSNVAVORDAPLEYDVSQVORLQVLE 85
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 85 LKE-----IVNLSKSCQCKQADNDGPGRNGLLLPSTGAPGEVCN----- 128
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
D5 86 IMENNTQWLKLENYIQDNMKKEMVEIQNAVQN-----QTAVMIEIGTNLLNQ 134
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 129 -----RVRELESEV-----NKLSELKNAKEE--NVLHGR---LEKL 161
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
D5 135 TAEOTRKLTDVEAQLNQT*RLLEQLLEHSLSTNKLKQILDQTSINKLQDKNSFLEKK 194
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 162 NLV-----NMNNIENYVDKSVANLTF-----V 183
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
D5 195 VLAMEDKHIIQLQS:KEEKDQLVLVSKQNSI:EELEKKIVTATVNSVLQKQOHDLMET 254
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 184 VNSLDGKSCKPSQEQIQSRPVQHLYKDCSDYYAIGKRSSEYRVTPDPKNSSEFYVCD 243
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
D5 255 VNNLLTWMTSNAKPTVAKEQISFRDCAEVFKSGHTNGIYTLTFNTEBIAKAYCD 314
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 244 METMGGGWTVLQARLDGSTNFTRTWQDYKAGFNLRRREFWLGNDKIHLLTKSKEMILRID 303
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
D5 315 MEAGGGWTIIQRREDGSDVDFORTWKEYKVGFGNPSGEYWLGNFVSLTNQORYVLKIH 374
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 304 LEDFNGVELYALYQFYVANEFLKYRLHVGNYNGTAGDALRFNKHYNHDLKFFTPDKDN 363
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
D5 375 LKDWEGNEAVSLYEHFVLSSEELNRYIHLKGLTGTAGKISSISQPGND----FSTKQDGN 430
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 364 DRYPSGNCGLYSSGWMFQACLSANLNGKYHOKYGVGR--NGIFMGWPGVSEAHPSGYK 422
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
D5 431 DKCIC-KCSQMLTGGWAFDAGPSNLNGYYPQONTNKFNGIKYIWKG-----SGY- 482
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 423 SSFKEAKNMIRPKHF 437
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
D5 483 -SLKATTMMIRPADF 496
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

RESULT 15
US-09-351-543-4
; Sequence 4, Application US/09351:543
; Patent No. 6436693
; GENERAL INFORMATION:
; APPLICANT: THORPE, PHILIP E.
; APPLICANT: RAN, SOPHIA
; TITLE OF INVENTION: CANCER TREATMENT METHODS USING ANTIBODIES TO
; TITLE OF INVENTION: AMINO PHOSPHOLIPIDS
; FILE REFERENCE: 4001.002200
; CURRENT APPLICATION NUMBER: US/09/351,543
; CURRENT FILING DATE: 1999-07-12
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
; LENGTH: 496
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-351-543-4

Query Match      22.0%; Score 522; DB 4; Length 496;
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```

Best Local Similarity 27.9%; Pred. No. 1.2e-39;
Matches 138; Conservative 74; Mismatches 159; Indels 124; Gaps 15;

QY 43 LESRGKCE---EAGECPYQVSJPLP-----TIQ--LPKQFSR:EEVFKEVON 84
   |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
Db 26 MDSIGKKQYQVQHSGCSYTFLLPENDCNCRSSSPYVSNVQRCAPLEYDSDVQR-QVLEN 85
   |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
QY 85 LKE-----IVNSLKSCQCCKLQADDNGDPGRNGULLPSTGAPGEVGN----- 128
   |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
Db 86 INENNTQWLMLKENYIQNNYKKEVMEIQQNAVQN-----QTAVMIEIGTNELNO 134
   |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
QY 129 -----RVRELESEV-----NKLSELKNAKEEINVLGR---LEKL 161
   |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
Db 135 TAEQTRKLTQVLAQVLNQTTRELEQLLEHSLSTNLEKQILDQTSINKLQDKNSFLEKK 194
   |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
QY 162 NLV-----NNNIENYVDSKVANLTF-----V 183
   |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
Db 195 VLAVEDKHIIQOSIKEEKQQLVLVSKQNSIIELEKKIVTATVNNSVLQKQCHLNET 254
   |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
QY 184 VNSLDGKCKSCPSOIOISRPVQHLYIKDCSDYYAIGKPSSETYRVTPDPKNSSEVYCD 243
   |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
Db 255 VANLLTMMSTNSAKDPTVAKEEQISFRDCAEVFKSGHTTNGIYTLTFNSTEEIKAYCD 314
   |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
QY 244 METMGSGWTVLQARLQGSTNFTQDYKAGFGNLRREFWLQNDKIHLLTKSKEMILRID 302
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Db 315 MEAGGGGWTIIORREDGSYDFQRTWKEYKVGFGNPSGEYKLGNEFVSQLTQORYVLXIH 374
   |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
QY 304 LEDFNGVELYALDOFYVANEFKYRLJHGVNNGTAGDALRPNKHYNHLEKFTTTPDKEN 363
   |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
Db 375 LKDWEGNEAYSLYEHFYLSEELNYRIH-LGLTG*AGK:SSISQFGND----FSTKDCGN 430
   |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
QY 364 DRYPSCNCGLYYSSGWMFDACLSANLNGKYHOKYAGYR-NGIFWGTWPGVSEAHPGGYK 422
   |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
Db 431 DKCIC-KCQMUTGGWMPDACCPSNLNGMYYPQRCNTNKFNGIKWYKRG-----SGY- 482
   |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
QY 423 SSFKEAKMMIRPKHF 437
   |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
Db 483 -SJKATTMMIRPADF 496
   |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||

```

Search completed: November 5, 2003, 16:48:59
Job time : 32.9427 secs

GenCore version 5.1.6
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CM protein - protein search, using sw model

Run on: November 5, 2003, 16:39:17 ; Search time 0.92511 Seconds
(without alignments)
1559.306 Million cell updates/sec

Title: US-09-902-563-18

Perfect score: 88

Sequence: 1 DRYPSGNCGLYYSSG 15

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283308 seqs, 3616692 residues

Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : PIR 76:*

1: PIR1:*

2: PIR2:*

3: PIR3:*

4: PIR4:*

pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARY-ES

Result No.	Score	Query Match	Length	DB ID	Description
1	88	100.0	432	2 I56934	fibrinogen-like pr
2	98	100.0	432	2 A27447	cytotoxic T-lympho
3	99	100.0	439	2 I37391	fibrinogen-like pr
4	46	52.3	2403	2 A59186	sanko - human
5	46	52.3	3461	2 S58870	ree-in precursor -
6	43	48.9	225	2 C82893	hypothetical prote
7	43	48.9	284	2 I49707	germ cell specific
8	43	48.9	339	2 T24007	hypothetical prote
9	43	48.9	456	2 C86624	hypothetical prote
10	43	48.9	456	2 R72000	hypothetical prote
11	42.5	48.3	696	2 G71829	probable outer mem
12	41	46.6	273	2 T4246	hypothetical prote
13	41	46.6	368	2 A81289	hypothetical prote
14	41	46.6	395	2 T26404	hypothetical prote
15	41	46.6	437	2 A72513	hypothetical prote
16	41	46.6	517	1 ERADA7	early E2A DNA-bind
17	41	46.6	591	1 WMBPQ2	gene P2 protein -
18	41	46.6	680	2 H70347	outer membrane pro
19	41	46.6	798	2 T00131	xylan 1,4-beta-xy
20	40	45.5	92	2 A72242	ferredoxin - Therm
21	40	45.5	100	2 JN0734	hypothetical 11.49
22	40	45.5	165	2 D86894	hypothetical prote
23	40	45.5	245	2 G64210	uracil DNA glycosy
24	40	45.5	286	2 A33546	actin-capping prot
25	40	45.5	294	2 AF3043	calcium-binding pr
26	40	45.5	305	2 P98242	regucalcin (AB0379
27	40	45.5	455	2 E64454	proline-trna ligas
28	40	45.5	474	2 ERAD41	early E2A DNA-bind
29	40	45.5	484	2 ERAD12	early E2A DNA-bind

ALIGNMENTS

RESULT 1

56934
fibrinogen-like protein - mouse
C:Species: Mus sp. (mouse)
C>Date: 26-Jul-1996 #sequence_revision 26-Jul-1996 #text_change 03-Dec-1999
C:Accession: I56934
R:Patr. R.L.: Fung, L.; Reneker, J.; Myers-Mascen, N.; Leibowitz, J.; Levy, G.
J. Virol. 69, 5033-5038, 1995
A>Title: Association of mouse fibrinogen-like protein with murine hepatitis virus-indu
A:Reference number: 56934; MJID:95333285; PMID:7609073
A:Accession: I56934
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-432 <RES>
A:Cross-references: GB:S78773; NID:glc42169; PID:AA34823.1; PID:G:042170
C:Gene: mufiblp
C:Superfamily: fibrinogen gamma chain; fibrinogen beta/gamma homology
F:203-428/Domain: fibrinogen beta/gamma homology <FBG>

Query Match 100.0%; Score 88; DB 2; Length 432;
Best Local Similarity 100.0%; Pred. No. 2.1e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 3; Gaps 0;

QY : DRYPSGNCGLYYSSG 15
| | | | | | | | | | | | | | | |
Db 357 DRYPSGNCGLYYSSG 371

RESULT 2

A27447
cytotoxic T-lymphocyte-specific protein precursor (clone pT49); - mouse
C:Species: Mus musculus (house mouse)
C>Date: 15-Dec-1998 #sequence_revision 15-Dec-1998 #text_change 03-Dec-1999
C:Accession: A27447
R:Koyama, T.; Hall, L.R.; Haseg, W.G.; Toneyawa, S.; Saito, H.
Proc. Natl. Acad. Sci. U.S.A. 84, 1609-1613, 1987
A>Title: Structure of a cytotoxic T-lymphocyte-specific gene shows a strong homology t
A:Reference number: A27447; MUID:87175527; PMID:3550794
A:Accession: A27447
A:Molecule type: mRNA
A:Residues: 1-432 <KOT>
A:Cross-references: GB:M16238; NID:gl93304; PID:AA37624.1; PID:g387156
C:Superfamily: fibrinogen gamma chain; fibrinogen beta/gamma homology
F:203-428/Domain: fibrinogen beta/gamma homology <FBG>

Query Match 100.0%; Score 88; DB 2; Length 432;
Best Local Similarity 100.0%; Pred. No. 2.1e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 3; Gaps 0;

OY 1 DRYPSGNCGLYYSSG 15
| | | | | | | | | | | | | | | |

D3 357 DRYPSGNCGLYSSG 371

RESULT 3

I37391

C:Species: Homo sapiens (man)

C:Date: 31-Nov-1996 #sequence_revision 01-Nov-1996 #text_change 21-Jul-2000

C:Accession: I37391; S47273

R:Ruegg, C.; Pytel, R.

Gene 160, 257-262, 1995

A:Title: Sequence of a human transcript expressed in T-lymphocytes and encoding a fibrin

A:Reference number: I37391; MUID:95369700; PMID:7642136

A:Accession: I37391

A>Status: preliminary; translated from GB/EMBL/DDBJ

A:Molecule type: mRNA

A:Residues: 1-439 <RES>

A:Cross-references: EMBL:Z36531; NID:3535184; PIDN:GA085298.1; PID:9535185

A:Note: Submitted to the EMBL Data Library, August 1994

C:Superfamily: fibrinogen gamma chain; fibrinogen beta/gamma homology

F:210-435/Domain: fibrinogen beta/gamma homology <FBG>

Query Match 100.0%; Score 88; DB 2; Length 439;

Best Local Similarity 100.0%; Pred. No. 2,1e-06; Mismatches 0; Indels 0; Gaps 0;

QY 1 DRYPSGNCGLYSSG 15

|||||

D3 364 DRYPSGNCGLYSSG 378

RESULT 4

A59386

sacko - human

C:Species: Homo sapiens (man)

C:Date: 31-Dec-2001 #sequence_revision 31-Dec-2001 #text_change 31-Dec-2001

C:Accession: A59386

R:Ranko, S.

Submitted to the Protein Sequence Database, March 2001

A:Reference number: A59386

A:Accession: A59386

A>Status: preliminary

A:Molecule type: protein

A:Residues: 1-2403 <SAN>

Query Match 52.3%; Score 46; DB 2; Length 2403;

Best Local Similarity 64.3%; Pred. No. 54; Mismatches 2; Indels 1; Gaps 1;

QY 4 PSQNCGLYSSG 15

|||||

D3 1752 PSQNCGLYSSG 1765

RESULT 5

S58870

reelin precursor - mouse

C:Species: Mus musculus (house mouse)

C:Date: 06-Dec-1996 #sequence_revision 06-Dec-1996 #text_change 11-Jan-2000

C:Accession: S58870; S71844; I49297

R:D'Arcangelo, G.; Mao, G.G.; Chen, S.C.; Soares, H.D.; Morgan, J.L.; Curran, T.

Nature 374, 719-723, 1995

A:Title: A protein related to extracellular matrix proteins deleted in the mouse mutant

A:Reference number: I49297; MUID:95231649; PMID:7715726

A:Accession: S58870

A>Status: nucleic acid sequence not shown

A:Molecule type: mRNA

A:Residues: 1-3461 <DAR>

A:Cross-references: EMBL:U24703; NID:9902496; PID:9902487

R:D'Arcangelo, G.

Submitted to the EMBL Data Library, April 1995

A:Reference number: S71844

A:Accession: S71844

A:Molecule type: mRNA

A:Residues: 1-215, 'V', 217-1905, 'S', 1907-3355, 'V', 3357-3391, 'N', 3393-3461 <DA2>

A:Cross-references: EMBL:U24703; NID:9902486; PID:9902487

C:Superfamily: unassigned EGF-related proteins; EGF homology

F:1-27/Domain: signal sequence #status predicted <SIG>

F:28-346//Product: reelin #status predicted <MAT>

F:1769-1795/Domain: EGF homology <EGF>

Query Match 52.3%; Score 46; DB 2; Length 3461;

Best Local Similarity 71.4%; Pred. No. 76; Mismatches 10; Conservative 0; Indels 2; Gaps 1;

QY 3 YPSGNCGLY--YSS 14

|||||

D3 1974 YPSGNCGLYCPYSS 1987

RESULT 6

C82893

hypothetical protein U425 [imported] - Ureaplasma urealyticum

C:Species: Ureaplasma urealyticum

C:Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 20-Aug-2000

C:Accession: C82893

R:Glass, J.L.; Lefkowitz, E.J.; Glass, J.S.; Heiner, C.R.; Chen, E.Y.; Casselli, G.H.

Submitted to GenBank, February 2000

A:Description: The complete sequence of Ureaplasma urealyticum: Alternate views of a

A:Reference number: A82870

A:Accession: C82893

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-225 <GLA>

A:Cross-references: GB:AE002139; GB:AF222894; NID:96899405; PIDN:AAF30837.1; GSPDB:GNO

A:Experimental source: serovar 3; biovar 1

C:Genetics:

A:Gene: U425

A:Genetic code: SGC3

Query Match 48.9%; Score 43; DB 2; Length 225;

Best Local Similarity 70.0%; Pred. No. 18; Mismatches 7; Conservative 1; Indels 2; Gaps 0;

QY 3 YPSGNCGLY 12

|||||

D3 87 YPSGNCGLY 96

RESULT 7

I49707

germ cell specific gene 3 protein - mouse

C:Species: Mus musculus (house mouse)

C:Date: 29-May-1998 #sequence_revision 29-May-1998 #text_change 19-May-2000

C:Accession: I49707

R:Tanaka, H.; Yoshimura, Y.; Nishina, Y.; Nozaki, M.; Nojima, H.; Nishimura, Y.

FEBS Lett. 355, 4-10, 1994

A:Title: Isolation and characterization of cDNA clones specifically expressed in testis

A:Reference number: I49707; MUID:95046372; PMID:7937958

A:Accession: I49707

A>Status: preliminary; translated from GB/EMBL/DDBJ

A:Molecule type: mRNA

A:Residues: 1-284 <RES>

A:Cross-references: GB:D38545; NID:9603492; PID:9603493

C:Superfamily: actin-capping protein alpha chain

Query Match 48.9%; Score 43; DB 2; Length 284;

Best Local Similarity 60.0%; Pred. No. 22; Mismatches 6; Conservative 2; Indels 2; Gaps 0;

QY 1 DRYPSGNCGL 10

|||||

D3 13: DRYPSGNCGL 140

RESULT 8

```

T24007
Hypothetical protein R07B5.7 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C>Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 21-Jul-2000
C:Accession: T24007
R:Kelly, P.
Submitted to the EMBL Data Library, May 1996
A:Reference number: Z39829
A:Accession: T24007
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-339 <WL>
A:Cross-references: EMBL:Z72512; PIDN:CAA96667.1; GSPDB:GN5C023; CESP:R07B5.7
A:Experimental source: clone R07B5
C:Genetics:
A:Gene: CESP:R07B5.7

A:Map position: 5
A:Introns: 31/2; 93/1; 124/3; 194/3; 247/3; 267/3
C:Superfamily: Caenorhabditis elegans hypothetical protein C33A12.9b

Query Match 48.9%; Score 43; DB 2; Length 339;
Best Local Similarity 53.8%; Pred. No. 26;
Matches 7; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 3 YPSGNCGLYSSG 15
      |||
DB 232 YPFGSVSVYSSG 244
      |||

RESULT 9
C86624
Hypothetical protein CPJ070 [imported] - Chlamydophila pneumoniae (strain J138;
C:Species: Chlamydophila pneumoniae; Chlamydia pneumoniae
C>Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 02-Mar-2001
C:Accession: C86624
R:Shirai, M.; Hirakawa, H.; Kimoto, M.; Tabuchi, M.; Kishi, F.; Ouchi, K.; Shiba, T.; Ise
Nucleic Acids Res. 28, 2311-2314, 2000
A:Title: Comparison of whole genome sequences of chlamydia pneumoniae J138.
A:Reference number: A86491; MUID:20330349; PMID:10871362
A:Accession: C86624
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-456 <STO>
A:Cross-references: GB:BA000028; NID:98979443; PIDN:BAH99277.1; GSPDB:GN5C0-42
A:Experimental source: strain J138
C:Genetics:
A:Gene: CPJ070

Query Match 48.9%; Score 43; DB 2; Length 456;
Best Local Similarity 60.0%; Pred. No. 34;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 3 YPSGNCGLYSSG 12
      |||
DB 3 FPGNCNCYY 12
      |||

RESULT 10
H72000
Hypothetical protein CP0780 [imported] - Chlamydophila pneumoniae (strains CWL029 and AR
C:Species: Chlamydophila pneumoniae; Chlamydia pneumoniae
C>Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 11-May-2000
C:Accession: H72000; A81538
R:Kalan, S.; Mitchell, W.; Marathe, R.; Jammel, C.; Fan, C.; Clinger, L.; Grimwood, C.;
Nature Genet. 21, 385-389, 1999
A:Title: Comparative genomes of Chlamydia pneumoniae and C. trachomatis.
A:Reference number: A72000; MUID:99206666; PMID:10192388
A:Accession: H72000
A:Molecule type: DNA
A:Residues: 1-456 <ARN>
A:Cross-references: GB:AE001687; GB:AE001363; NID:94377396; PIDN:AAI19227.1; PID:9437740
A:Experimental source: strain CWL029
R:Read, T.D.; Brunham, R.C.; Shen, C.; Gill, S.R.; Heideberg, J.F.; White, O.; Hickey,

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, C.; Dodson, R.; Gwinn, M.; Nelson, W.; DeBoy, R.; Kolonay, J.; McClarty, G.; Saizber
Nucleic Acids Res. 28, 1397-1406, 2000
A:Title: Genome sequences of Chlamydia trachomatis Mogen and Chlamydia pneumoniae AR39.
A:Reference number: A81500; MUID:20150255; PMID:10684935
A:Accession: A81538
A:Molecule type: DNA
A:Residues: 1-456 <REA>
A:Cross-references: GB:AE002238; GB:AE002161; NID:97189693; PIDN:AAF38579.1; PID:97189
A:Experimental source: strain AR39, HL cells
C:Genetics:
A:Gene: CPN1070; CP0780

Query Match 48.9%; Score 43; DB 2; Length 456;
Best Local Similarity 60.0%; Pred. No. 34;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 3 YPSGNCGLYSSG 12
      |||
DB 3 FPGNCNCYY 12
      |||

RESULT 11
G71829
Probable outer membrane protein - Helicobacter pylori (strain J99)
C:Species: Helicobacter pylori
A:Variety: strain J99
C:Accession: G71829; G71960
C>Date: 12-Feb-1999 #sequence_revision 12-Feb-1999 #text_change 08-Oct-1999
R:Am, R.A.; Ling, L.S.L.; Voir, D.T.; King, B.L.; Brown, E.D.; Doig, P.C.; Smith, D.R.
J. Ves, C.; Gibson, R.; Merberg, D.; Mills, S.D.; Jiang, Q.; Taylor, D.E.; Vovis, S.F.
Nature 397, 176-180, 1999
A:Title: Genomic sequence comparison of two unrelated isolates of the human gastric pa
A:Reference number: A71800; MUID:99120557; PMID:9923682
A:Accession: G71829
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-696 <ARN>
A:Cross-references: GB:AE001549; GB:AE001439; NID:94155858; PIDN:AAD38834.1; PID:94155
A:Experimental source: strain J99
A:Accession: G71960
A:Molecule type: DNA
A:Residues: 1-696 <AR2>
A:Cross-references: GB:AE001459; GB:AE001439; NID:94154723; PIDN:AAD35786.1; PID:94154
A:Experimental source: strain J99
C:Genetics:
A:Gene: Jhp02.2

Query Match 48.3%; Score 42.5; DB 2; Length 696;
Best Local Similarity 69.2%; Pred. No. 61;
Matches 9; Conservative 0; Mismatches 3; Indels 1; Gaps 1;

QY 3 YPSGNCGLYSSG 15
      |||
DB 231 YPDSN-GNYSSG 242
      |||

RESULT 12
T16246
Hypothetical protein F35A5.4 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C>Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 18-Feb-2000
C:Accession: T16246
R:Leimbach, D.
Submitted to the EMBL Data Library, January 1996
A:Description: The sequence of C. elegans cosmid F35A5.
A:Reference number: Z18485
A:Accession: T16246
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-273 <LEI>
A:Cross-references: EMBL:U46675; NID:91166613; PID:91166614; PIDN:AAB52645.1; GSPDB:GN
A:Experimental source: strain Bristol N2; clone F35A5
C:Genetics:

```

A:Gene: CESP:F35A5.4

A:Map position: X

A:Introns: 18/3; 62/3; 81/3; 100/3; 140/3; 226/2

Query Match 46.6%; Score 41; DB 2; Length 273;

Best Local Similarity 66.7%; Pred. No. 44;

Matches 8; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 4 PSNGCGLYYSSG 15

DB 50 PSNGCGCGSCG 61

RESULT 13

A81289 hypothetical protein Cj1433c (imported) - Campylobacter jejuni (strain NCTC 11168)

C:Species: Campylobacter jejuni

C>Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change C3-Jun-2002

C:Accession: A81289

R:Parkhill, J.; Wren, B.W.; Mungall, K.; Kealey, J.M.; Churcher, C.; Basham, D.; Chilling

C.W.; Quail, M.; Rajandream, M.A.; Rutherford, K.M.; VanVleet, A.; Whitehead, S.; Barr

Nature 403, 665-668, 2003

A:Title: The genome sequence of the food-borne pathogen Campylobacter jejuni reveals hyd

A:Reference number: A81250; MUID:20150912; PMID:10669204

A:Accession: A81289

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-368 <PAR>

A:Cross-references: GB:AL119378; GB:AL111168; NID:G6968723; PIDN:CAB71857.1; PID:969888

A:Experimental source: serotype O2, strain NCTC 11168

C:Genetics:

A:Gene: Cj1433c

C:Superfamily: Campylobacter jejuni hypothetical protein Cj1433c

Query Match

Best Local Similarity 46.6%; Score 41; DB 2; Length 368;

Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 4 PSNGCGLYYS 13

DB 265 PSNGCDNVHS 274

RESULT 14

T26404

hypothetical protein Y105CSB.bb - Caenorhabditis elegans

C:Species: Caenorhabditis elegans

C>Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 20-Jun-2000

C:Accession: T26404

R:McMurray, A.

submitted to the EMBL Data Library, September 1999

A:Reference number: Z20208

A:Accession: T26404

A:Status: preliminary; translated from GB/EMBL/DBEB

A:Molecule type: DNA

A:Residues: 1-385 <WIL>

A:Cross-references: EMBL:AL110479; PIDN:CAB54376.1; CESP:Y105CSB.bb

A:Experimental source: Clone Y105CSB

C:Genetics:

A:Gene: CESP:Y105CSB.bb

A:Introns: 58/1; 112/1; 270/2

C:Superfamily: glutamate-ammonia ligase

Query Match

Best Local Similarity 46.6%; Score 41; DB 2; Length 355;

Matches 8; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

QY 1 DRPSGNCGLYYSSG 15

DB 341 DRPSNCDFYTVTC 355

RESULT 15

A72513

hypothetical protein APE2078 - Aeropyrum pernix (strain K1)

C:Species: Aeropyrum pernix

C>Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 20-Jun-2000

C:Accession: A72513

R:Kawarabayashi, Y.; Hino, Y.; Horikawa, H.; Yamazaki, S.; Haikawa, Y.; Jin-no, K.; Takawa, H.; Takamiya, M.; Masuda, S.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, C.; DNA Res. 6, 83-101, 1999

A:Title: Complete genome sequence of an aerobic hyper-thermophilic Crenarchaeon, Aerof

A:Reference number: A72450; MUID:99310339; PMID:10382966

A:Accession: A72513

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-437 <RAW>

A:Cross-references: DDBJ:AP000063; NID:G5105654; PIDN:BAA91089.1; PID:G5105777

A:Experimental source: strain K1

C:Genetics:

A:Gene: APE2078

C:Superfamily: conserved hypothetical protein NTH1394

Query Match

Best Local Similarity 46.6%; Score 41; DB 2; Length 437;

Matches 8; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 2 RYPSGNCGLYYSSG 15

DB 112 RYVEGEAGLYSSG 125

Search completed: November 5, 2003, 16:48:15

Job time : 2.92511 secs

GenCore version 5.1.1.6
Copyright: (c) 1993 - 2003 Compugen Ltd.

OK protein - protein search, using sw model

Run on: November 5, 2003, 15:59:02 ; Search time 0.560793 Seconds
(without alignments)
1067.506 Million cell updates/sec

Title: US-09-902-563-18

Perfect score: 88

Sequence: 1 DRYPSGNCGLYSSG 15

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 6

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 9%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_41.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	88	100.0	432	1	FGL2_MOUSE	P12804 Mus musculus
2	88	100.0	439	1	FGL2_HUMAN	Q14314 homo sapien
3	46	52.3	3209	1	RELN_CHICK	O91574 gallus gall
4	46	52.3	3460	1	RELN_HUMAN	P93569 homo sapien
5	46	52.3	3421	1	RELN_MOUSE	Q60841 mus musculus
6	46	52.3	3462	1	RELN_RAT	P58751 rattus norv
7	45	51.1	210	1	BCA3_HUMAN	Q96kx2 homo sapien
8	43	48.9	299	1	CAZ3_HUMAN	P70190 mus musculus
9	43	48.9	299	1	CAZ3_MOUSE	P70190 mus musculus
10	43	48.9	299	1	CAZ3_RAT	Q94wv6 rattus norv
11	41	46.6	121	1	CHAB_LYMDI	P50603 lymantria d
12	41	46.6	437	1	YK78_AERPE	Q94d60 aeropyrum p
13	41	46.6	488	1	CTAC_HUMAN	P04497 human adeno
14	41	46.6	517	1	DNB2_ADE07	P04497 human adeno
15	41	46.6	530	1	VPC2_BPRD	P27378 bacterioph
16	40	45.5	245	1	UNC_XYCGE	P47343 mycoplasma
17	40	45.5	286	1	CAZ1_CHICK	P13127 gallus gall
18	40	45.5	455	1	SYPC_METJA	Q59635 methanococc
19	40	45.5	474	1	DNB2_ADE41	P11807 human adeno
20	40	45.5	484	1	DNB2_ADE12	P04498 human adeno
21	40	45.5	776	1	AD07_MACFA	Q28475 macaca fasc
22	40	45.5	121	1	ATH1_YEAST	P48016 saccharomyc
23	39.5	44.9	1391	1	LYS2_CANAL	Q12572 candida alb
24	39	44.3	78	1	R27A_ASPOF	P31753 asparagus o
25	39	44.3	79	1	R27A_HORVU	P22277 hordeum vul
26	39	44.3	79	1	R27A_MAZE	P27923 zea mays lm
27	39	44.3	80	1	R27A_LYCES	P27923 lycopersico
28	39	44.3	81	1	27AB_ARATH	P59232 arabidopsis
29	39	44.3	81	1	27AC_ARATH	P59233 arabidopsis
30	39	44.3	212	1	BCA3_MOUSE	Q94wv6 mus musculu
31	39	44.3	420	1	Y461_SYNY3	Q55167 synechocyst
32	39	44.3	754	1	AD07_HUMAN	Q94h29 homo sapien
33	39	44.3	832	1	SM4B_HUMAN	Q94npr2 homo sapien

RESULT 1

FGL2_MOUSE
ID FG_L2_MOUSE STANDARD; PRT; 432 AA.
AC P12804;
DT C1-CCT-1989 (Rel. 12, Created)
DT 01-CCT-1989 (Rel. 12, Last sequence update)
DT 16-CCT-2001 (Rel. 40, Last annotation update)
DE Fibroleukin precursor (Fibrinogen-like protein 2) (Prothrombinase)
DE (Cytotoxic T-lymphocyte specific protein).
GN FGL2 OR FIBLP.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognath; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Cytotoxic T-cell;
RX MEDLINE=8717527; PubMed=3550794;
RA Koyama T., Hall L.R., Hasegawa S., Saito H.;
RT "Structure of a cytotoxic T-lymphocyte-specific gene shows a strong
RT homology to fibrinogen beta and gamma chains";
RJ Proc. Natl. Acad. Sci. U.S.A. 84:1609-1613(1987).
RN [2]
RP SEQUENCE FROM N.A., AND CHARACTERIZATION.
RC STRAIN=BAJL/CJ; TISSUE=Peritoneal macrophage;
RX MEDLINE=95333285; PubMed=7609073;
RA Parr R.L., Fung L., Reneker J., Myers-Yason N., Leibowitz J.L.,
RA Levy G.;
RT "Association of mouse fibrinogen-like protein with murine hepatitis
RT virus-induced prothrombinase activity";
RJ J. Virol. 69:5033-5038(1995).
CC -!- FUNCTION: CONVERTS PROTHROMBIN TO THROMBIN.
CC -!- SUBUNIT: HOMOTETRAMER; DISULFIDE-LINKED (BY SIMILARITY).
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: CONSTITUTIVELY EXPRESSED IN CYTOTOXIC
CC T-CELLS.
CC -!- INDUCTION: IN MACROPHAGES, DURING INFECTION BY MOUSE HEPATITIS
CC VIRUS STRAIN 3 (MHV-3).
CC -!- SIMILARITY: Contains 1 fibrinogen C-terminal domain.
CC
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CC or send an email to license@isb-sib.ch).
CC
CC EMBL; M16238; AAA37624.1;
CC EMBL; M15761; AAA37624.1; JOINED.
CC EMBL; S78773; AAB34823.1;
CC FIR; A27447; A27447.
CC HSP; P02671; IFZD.
CC MGS; MG1:103266; Fgl2.
CC InterPro; IPR002181; Fibrinogen_C.
CC Pfam; PF00147; fibrinogen_C_1.

ALIGNMENTS

34	39	44.3	1077	1	XYNY_CLOTR
35	39	44.3	1215	1	C-KA_BACTM
36	38	43.2	322	1	PSA_BRARE
37	38	43.2	323	1	HEM2_SCHPO
38	38	43.2	365	1	GLN2_DROME
39	38	43.2	367	1	GLNA_CAEEL
40	38	43.2	373	1	GLNA_MOUSE
41	38	43.2	373	1	GLNA_RAT
42	38	43.2	399	1	GLN1_DROME
43	38	43.2	401	1	COAT_PAV
44	38	43.2	403	1	GLNA_SQUAC
45	38	43.2	486	1	DNAB_RICPR

P51584 clostridium
Q45715 bacillus th
Q9YHV4 brachydanio
P78974 schizosacch
P2C478 drosophila
P34497 caenorhabdi
P51105 mus musculu
P09606 rattus norv
P2C477 drosophila
Q9J720 pariaceto v
P41320 squalius aca
Q9ZD08 rickettsia

```
DR SMART; SMC0186; FBG; 1.
DR PROSITE; PS00514; FIBRIN AG C-TERMINAL; 1.
KW T-cell; Cytolysis; Signal.
FT SIGNAL 1 19 POTENTIAL.
FT CHAIN 20 432 FIBROLEUKIN.
FT DOMAIN 203 428 FIBRINOGEN C-TERMINAL.
FT DISULFID 206 235 BY SIMILARITY.
FT DISULFID 364 377 BY SIMILARITY.
FT CARBOHYD 24 24 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 172 172 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 228 228 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 256 256 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 329 329 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CONFLICT 332 332 A -> G (IN REF. 2).
SQ SEQUENCE 432 AA; 48951 MW; 28297F69CCB4A782 CRC64;

Query Match 100.0%; Score 88; DB 1; Length 432;
Best Local Similarity 100.0%; Pred. No. 8.2e-07;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DRYPSGNCGLYSSG 15
D5 357 DRYPSGNCGLYSSG 371

RESULT 2
FG12 HUMAN STANDARD; PRT; 439 AA.
AC Q14314;
DT 16-OCT-2001 (Ref. 40, Created;
DT 16-OCT-2001 (Ref. 40, Last sequence update;
DT 15-SEP-2003 (Ref. 42, Last annotation update)
DE Fibrinoleukin precursor (Fibrinogen-like protein 2) (p749).
GN FGL2.
CS Homo sapiens (Human).
CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
CC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
CX KCB; TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Small intestine;
RX MEDLINE=95369700; PubMed=7642106;
RA Ruegg C., Pytel A. R.;
RT "Sequence of a human transcript expressed in T-lymphocytes and
RT encoding a fibrinogen-like protein.";
RJ Gene 160:257-262(1995).
RN [2]
RP SEQUENCE FROM N.A.
RA Yuvaraj S., Liu M., Marsden P., Levy G.;
RT "Cloning and characterization of Hfgl2: the human counterpart to the
RT mouse gene Fgl2.";
RJ Submitted (NOV-1998) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A., AND VARIANT GLU-53.
RA Rieder M.C., Armet T.Z., Carrington D.P., Chung M.-w., Lee K.-b.,
RA Poel C.L., Ozuna M., Y. Q., Nickerson D.A.;
RJ Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A.
RC TISSUE=Blood;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Deje J.G.,
RA Klausner R.D., Collins P.S., Wagner J.E., Shenner C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Suetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.L., Wang J., Hsieh F.,
RA Dratchenko L., Matrusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Schreitz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Pearce C.,
RA Raba S.S., Loquellano N.A., Peters G.J., Abranson R.D., Mulhally S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gnarate P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.X., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Du X., Gibbs R.A.,
RA Fahy J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
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RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson W.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.B.,
RA Scerif A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length
RT human and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [5]
RX CHARACTERIZATION.
RX MEDLINE=95309432; PubMed=9647217;
RA Marazzi S., Blum S., Hartmann R., Gundersen D., Schreyer M.,
RA Argraves S., von Friedner V., Pytel A. R., Ruegg C.;
RT "Characterization of human fibroblast, a fibrinogen-like protein
RT secreted by T lymphocytes.";
RJ Immunol. 161:138-147(1998).
CC -!- FUNCTION: MAY PLAY A ROLE IN PHYSIOLOGIC LYMPHOCYTE FUNCTIONS AT
CC T-CELLS.
CC -!- SUBUNIT: HOMOTETRAMER; DISULFIDE-LINKED.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: CONSTITUTIVELY EXPRESSED IN CYTOTOXIC
CC T-CELLS.
CC -!- SIMILARITY: Contains 1 fibrinogen C-terminal domain.
CC
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CC
CC EMBL; Z36531; CA85298.1; .
CC EMBL; AF104015; AAD10825.1; .
CC EMBL; AF104014; AAD10825.1; JOINED.
CC EMBL; AF468959; AA168855.1; .
CC EMBL; BC033820; AA033820.1; .
CC F01; 137391; 137391.
CC HSSP; P02671; 1FZD.
CC Genew; HGNC:3696; FGL2.
CC MIM; 605351; .
CC GO; GO:000576; C:extracellular; TAS.
CC GO; GO:000573; C:fibrinogen beta chain; TAS.
CC GO; GO:0005974; C:fibrinogen gamma chain; TAS.
CC InterPro; IPR002181; Fibrinogen_C.
CC Pfam; PF00147; fibrinogen_C; 1.
CC SMART; SM00186; FBG; 1.
CC PROSITE; PS00514; FIBRIN AG C-TERMINAL.
KW T-cell; Glycoprotein; Signal; Polymorphism.
FT SIGNAL 1 23 POTENTIAL.
FT CHAIN 24 439 FIBROLEUKIN.
FT DOMAIN 213 435 FIBRINOGEN C-TERMINAL.
FT DISULFID 371 384 BY SIMILARITY.
FT DISULFID 371 384 BY SIMILARITY.
FT CARBOHYD 25 25 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 179 179 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 235 235 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 263 263 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 336 336 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT VARIANT 53 53 G -> E.
FT SEQUENCE 439 AA; 50228 MW; DF34656288E49568 CRC64;

Query Match 100.0%; Score 88; DB 1; Length 439;
Best Local Similarity 100.0%; Pred. No. 8.3e-07;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DRYPSGNCGLYSSG 15
D5 364 DRYPSGNCGLYSSG 378

RESULT 3
```

REELIN CHICK STANDARD; PRT; 3209 AA.

AC O93574;

DT 28-FEB-2003 (Rel. 41, Created)

DT 28-FEB-2003 (Rel. 41, Last sequence update)

DT 28-FEB-2003 (Rel. 41, Last annotation update)

DE Reelin (EC 3.4.21.-) (Fragment).

GN RELN.

OS Gallus gallus (Chicken).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae; Gallus.

OX NCBI_TaxID=9031;

RN [1]

RP SEQUENCE FROM N.A.

RA Bernier B., Goffinet A.M.;

RT Submitted (SEP-1998) to the EMBL/GenBank/DBJ databases.

CC -!- FUNCTION: Extracellular matrix serine protease that plays a role in layering of neurons in the cerebral cortex and cerebellum. Regulates microtubule function in neurons and neuronal migration. Affects migration of sympathetic preganglionic neurons in the spinal cord, where it seems to act as a barrier to neuronal migration. Enzymatic activity is important for the modulation of cell adhesion. Binding to the extracellular domains of lipoprotein receptors VLDLR and ApoER2 induces tyrosine phosphorylation of Dab1 and modulation of tau phosphorylation (By similarity).

CC -!- SUBUNIT: Binds to the ectodomains of VLDLR and ApoER2 (By similarity).

CC -!- SUBCELLULAR LOCATION: Secreted (By similarity).

CC -!- DOMAIN: The basic C-terminal region is essential for secretion (By similarity).

CC -!- SIMILARITY: BELONGS TO THE REELIN FAMILY.

CC -!- SIMILARITY: Contains 8 EGF-like domains.

CC -!- SIMILARITY: Contains 15 BNR repeats.

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CC -----

DR EMBL; AF090441; AAC35559.1; -

DR HSSP; P05106; 1JW2.

DR InterPro; IPR006289; EGF like.

DR InterPro; IPR002860; GH BNR.

DR InterPro; IPR006210; EGF.

DR Pfam; PF02012; BNR; 15.

DR Pfam; PF00008; EGF; 4.

DR SMART; SM0181; EGF; 5.

DR PROSITE; PS00022; EGF 1; 7.

DR PROSITE; PS01186; EGF 2; 7.

KW Hydrolase; Serine protease; Developmental protein; Matrix protein;

KW Cell adhesion; EGF-like domain; Glycoprotein; Repeat.

FT NON_TER 1 1

FT DOMAIN 418 449 EGF-LIKE 1.

FT DOMAIN 777 808 EGF-LIKE 2.

FT DOMAIN 1157 1190 EGF-LIKE 3.

FT DOMAIN 1513 1544 EGF-LIKE 4.

FT DOMAIN 1877 1909 EGF-LIKE 5.

FT DOMAIN 2226 2257 EGF-LIKE 6.

FT DOMAIN 2601 2632 EGF-LIKE 7.

FT DOMAIN 2976 3008 EGF-LIKE 8.

FT REPEAT 340 351 BNR 1.

FT REPEAT 546 557 BNR 2.

FT REPEAT 699 710 BNR 3.

FT REPEAT 904 915 BNR 4.

FT REPEAT 1070 1081 BNR 5.

FT REPEAT 1283 1294 BNR 6.

FT REPEAT 1434 1445 BNR 7.

FT REPEAT 1632 1643 BNR 8.

FT REPEAT 1791 1802 BNR 9.

FT REPEAT 1998 2009 BNR 10.

FT REPEAT 2147 2158 BNR 11.

FT REPEAT 2346 2357 BNR 12.

FT REPEAT 2526 2537 BNR 13.

FT REPEAT 2727 2738 BNR 14.

FT REPEAT 3111 3122 BNR 15.

FT DOMAIN 3180 3209 ARG-RICH (BASIC).

FT CARBOHYD 5 5 N-LINKED (GLCNAC. .) (POTENTIAL).

FT CARBOHYD 37 37 N-LINKED (GLCNAC. .) (POTENTIAL).

FT CARBOHYD 53 53 N-LINKED (GLCNAC. .) (POTENTIAL).

FT CARBOHYD 376 376 N-LINKED (GLCNAC. .) (POTENTIAL).

FT CARBOHYD 1014 1014 N-LINKED (GLCNAC. .) (POTENTIAL).

FT CARBOHYD 1195 1195 N-LINKED (GLCNAC. .) (POTENTIAL).

FT CARBOHYD 1348 1348 N-LINKED (GLCNAC. .) (POTENTIAL).

FT CARBOHYD 1669 1669 N-LINKED (GLCNAC. .) (POTENTIAL).

FT CARBOHYD 1893 1893 N-LINKED (GLCNAC. .) (POTENTIAL).

FT CARBOHYD 2017 2017 N-LINKED (GLCNAC. .) (POTENTIAL).

FT CARBOHYD 2065 2065 N-LINKED (GLCNAC. .) (POTENTIAL).

FT CARBOHYD 2317 2317 N-LINKED (GLCNAC. .) (POTENTIAL).

FT CARBOHYD 2710 2710 N-LINKED (GLCNAC. .) (POTENTIAL).

FT CARBOHYD 2764 2764 N-LINKED (GLCNAC. .) (POTENTIAL).

FT CARBOHYD 2821 2821 N-LINKED (GLCNAC. .) (POTENTIAL).

FT CARBOHYD 2933 2933 N-LINKED (GLCNAC. .) (POTENTIAL).

FT CARBOHYD 3160 3160 N-LINKED (GLCNAC. .) (POTENTIAL).

FT CARBOHYD 3187 3187 N-LINKED (GLCNAC. .) (POTENTIAL).

SQ SEQUENCE 3209 AA; 361288 MW; 81A7B6676BCAA3D1 CRC64;

Query Match 52.3%; Score 46; DB 1; Length 3209;

Best Local Similarity 71.4%; Pred. No. 34;

Matches 13; Conservative 2; Mismatches 2; Gaps 1;

QY 3 YPSGNGGLY--YSS 14

DE 1722 YPGNGIGLYCPYSS 1735

RESULT 4

RELN_HUMAN STANDARD; PRT; 3460 AA.

ID RELN_HUMAN

AC P78569; Q8UDQ2;

DT 28-FEB-2003 (Rel. 41, Created)

DT 28-FEB-2003 (Rel. 41, Last sequence update)

DT 28-FEB-2003 (Rel. 41, Last annotation update)

DE Reelin precursor (EC 3.4.21.-).

GN RELN.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

OX NCBI_TaxID=9606;

RN [1]

RP SEQUENCE FROM N.A. (ISOFORM 1).

RA MEDLINE=97202106; PubMed=9049633;

RA DeSilva U., D'Arcangelo G., Braden V.V., Chen J., Miao G.G., Curran T., Green E.D.;

RT "The human reelin gene: isolation, sequencing, and mapping on chromosome 7.";

RT Genome Res. 7:157-164(1997).

RN [2]

RP SEQUENCE OF 194-2556 FROM N.A.

RA Lamar B., Wamsley P., Gibson A., Maas J., Bauer C., Sapetti L.;

RL Submitted (JAN-1999) to the EMBL/GenBank/DBJ databases.

RN [3]

RP ALTERNATIVE SPLICING.

RX MEDLINE=99263436; PubMed=10328932;

RA Lambert de Rouvroit C., Bernier B., Royaux I., de Bergueyck V., Goffinet A.M.;

RT "Evolutionarily conserved, alternative splicing of reelin during brain development.";

RL Exp. Neurol. 156:229-238(1999).

RN [4]

RP DISEASE AND TISSUE SPECIFICITY.

RX MEDLINE=99080080; PubMed=9861036;


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FT CARBOHYD 2962 2961 N-LINKED (GLCNAC...) (POTENTIAL)
FT CARBOHYD 3015 3015 N-LINKED (GLCNAC...) (POTENTIAL)
FT CARBOHYD 3072 3072 N-LINKED (GLCNAC...) (POTENTIAL)
FT CARBOHYD 3104 3104 N-LINKED (GLCNAC...) (POTENTIAL)
FT CARBOHYD 3411 3411 N-LINKED (GLCNAC...) (POTENTIAL)
FT CARBOHYD 3438 3438 N-LINKED (GLCNAC...) (POTENTIAL)
FT VARSPPLIC 3428 3429 Missing (in isoform 2)
FT VARSPPLIC 3428 3460 Missing (in isoform 3)
FT VARSPPLIC 752 752 Missing (in isoform 3)
FT CONFLICT 752 752 E -> D (IN REF. 2)
FT CONFLICT 3460 AA; 389399 MW; 362COBA41SAB93C1 CRC64;
SQ SEQUENCE 3460 AA; 389399 MW; 362COBA41SAB93C1 CRC64;

Query Match 52.3%; Score 46; DB 1; Length 3460;
Best Local Similarity 71.4%; Pred. No. 37;
Matches 10; Conservative 0; Mismatches 2; Indels 2; Gaps 1;

Cy 3 YPSGNGCLY--YSS 14
Db 1973 YPGNGIGLYCPYSS 1986

RESULT 5
RELN MOUSE
ID RELN MOUSE STANDARD; PRT; 3461 AA.
AC Q60841; Q9CUA6; RELN; 3461 AA.
DT 28-FEB-2003 (Rel. 41; Last sequence update)
DT 28-FEB-2003 (Rel. 41; Last sequence update)
DE Reelin precursor (EC 3.4.21.-) (Reeler protein).
GN RELN OR RL.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
CX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORM 1).
RC TISSUE=Cerebellum;
RX MEDLINE=95231649; PubMed=7715726;
RA D'Arcangelo G., Miao G.G., Chen S.-C., Soares H.D., Morgan J.,
RA Curran T.,
RA "A protein related to extracellular matrix proteins deleted in the
RA mouse mutant reeler."
RA Nature 374:715-723(1995).
RN [2]
RP SEQUENCE FROM N.A. AND ALTERNATIVE SPLICING.
RX MEDLINE=98086481; PubMed=9417911;
RA Royaux I., Lambert de Rouvroit C., D'Arcangelo G., Denirov D.,
RA Goffinet A.M.,
RA "The reeler gene encodes a protein with an EGF-like motif expressed by
RA pioneer neurons."
RA Nat. Genet. 10:77-83(1995).
RN [3]
RP SEQUENCE OF 3044-3461 FROM N.A. (ISOFORM 2).
RC STRAIN=C57BL/6J; TISSUE=Testis;
RX MEDLINE=21085660; PubMed=11217851;
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamataka I.,
RA Saito T., Okaaki Y., Gojobori I., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Kasaiwa H.,
RA Fletschmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Schriml L.M., Stauble F., Suzuki R., Tomita M., Wagner L., Washio T.,

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RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake C., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi V.,
RA Gustincich S., Hill D., Hofmann V., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima C., Mazzarelli J., Mommaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA Wyrshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohsaki S.,
RA Hayaishizaki Y.,
RA "Functional annotation of a full-length mouse cDNA collection."
RT Nature 409:685-690(2001).
RN [3]
RP CHARACTERIZATION.
RX MEDLINE=97141547; PubMed=8987733;
RA D'Arcangelo G., Nakajima K., Miyata T., Ogawa M., Mikoshiba K.,
RA Curran T.,
RA "Reelin is a secreted glycoprotein recognized by the CR-50 monoclonal
RA antibody."
RT J. Neurosci. 17:23-31(1997).
RN [6]
RP CHARACTERIZATION.
RX MEDLINE=21634904; PubMed=11689558;
RA Quattrocchi C.C., Wamnes F., Persico A.M., Ciafre S.A.,
RA D'Arcangelo G., Farace M.G., Keller F.,
RA "Reelin is a serine protease of the extracellular matrix."
RN [7]
RP TISSUE SPECIFICITY.
RX MEDLINE=97325946; PubMed=9182958;
RA Schiffmann S.N., Bernier B., Goffinet A.M.,
RA "Reelin mRNA expression during mouse brain development."
RN [8]
RP ALTERNATIVE SPLICING AND TISSUE SPECIFICITY.
RX MEDLINE=99263436; PubMed=10328932;
RA Lambert de Rouvroit C., Bernier B., Royaux I., de Bergoyck V.,
RA Goffinet A.M.,
RA "Evolutionarily conserved, alternative splicing of reelin during brain
RA development."
RN [9]
RP BINDING TO VLDLR AND APOER2.
RX MEDLINE=20036019; PubMed=10571241;
RA Haesberger T., Trommsdorff V., Howell B.W., Goffinet A.M., Mumby V.C.,
RA Cooper J.A., Herz J.,
RA "Direct binding of Reelin to VLDLR receptor and ApoE receptor 2 induces
RA tyrosine phosphorylation of disabled-1 and modulates tau
RA phosphorylation."
RN [10]
RP FUNCTION.
RX MEDLINE=20359755; PubMed=10880573;
RA Yip J.W., Yip Y.P.L., Nakajima K., Capriotti C.,
RA "Reelin controls position of autonomic neurons in the spinal cord."
RN [11]
RP FUNCTION: Extracellular matrix serine protease that plays a role
in layering of neurons in the cerebral cortex and cerebellum.
Regulates microtubule function in neurons and neuronal migration.
Affects migration of sympathetic preganglionic neurons in the
spinal cord, where it seems to act as a barrier to neuronal
migration. Enzymatic activity is important for the modulation of
cell adhesion. Binding to the extracellular domains of lipoprotein
receptors VLDLR and ApoER2 induces tyrosine phosphorylation of
Dab1 and modulation of Tau phosphorylation.
CC -1- SUBUNIT: Binds to the ectodomains of VLDLR and ApoER2.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=3;
CC Name=1;
CC IsoId=Q60841-1; Sequence=Displayed;
CC Name=2;
CC IsoId=Q60841-2; Sequence=VSP_005577;

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CC CC Name=3;
 CC CC IsoId=O60841-3; Sequence=VSP_005578;
 CC CC -!- TISSUE SPECIFICITY: The major isoform 1 is neuron-specific. It is
 CC CC abundantly produced during brain ontogenesis by the Cajal-Retzius
 CC CC cells and other pioneer neurons located in the telencephalic
 CC CC marginal zone and by granule cells of the external granular layer
 CC CC of the cerebellum. Expression is located in deeper layers in the
 CC CC developing hippocampus and olfactory bulb. Low levels of
 CC CC expression are also detected in the immature striatum. At early
 CC CC developmental stages, expressed also in hypothalamic
 CC CC differentiation fields, tectum and spinal cord. A moderate to low
 CC CC level of expression occurs in the septal area, striatal fields,
 CC CC habenular nuclei, some thalamic nuclei, particularly the lateral
 CC CC geniculate, the retina and some nuclei of the reticular formation
 CC CC in the central field of the medulla. Very low levels found in
 CC CC liver and kidney. No expression in radial glial cells, cortical
 CC CC plate, Purkinje cells and inferior olivary neurons. The minor
 CC CC isoform 2 is only expressed in non-neuronal cells. The minor
 CC CC isoform 3 is found in the same cells as isoform 1, but is almost
 CC CC undetectable in retina and brain stem.
 CC CC -!- DEVELOPMENTAL STAGE: First detected at embryonic day 11.5.
 CC CC Expression increases up to birth and remains high from post-natal
 CC CC day 2 to 11 in both cerebellum and fore/midbrain. Expression
 CC CC declines thereafter and is largely brain specific in the adult.
 CC CC -!- DOMAIN: The basic C-terminal region is essential for secretion.
 CC CC -!- PTM: N-glycosylated and to a lesser extent also O-glycosylated.
 CC CC -!- DISEASE: Defects in reelin are the cause of the autosomal recessive
 CC CC reeler (rl) phenotype which is characterized by impaired motor
 CC CC coordination, tremors and ataxia. Neurons in affected mice fail to
 CC CC reach their correct locations in the developing brain, disrupting
 CC CC the organization of the cerebellar and cerebral cortices and other
 CC CC laminated regions.
 CC CC -!- SIMILARITY: BELONGS TO THE REELIN FAMILY.
 CC CC -!- SIMILARITY: Contains 8 EGF-like domains.
 CC CC -!- SIMILARITY: Contains 15 BNR repeats.
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 CC CC or send an email to license@sib-sib.ch).
 CC CC -----
 CC CC EMBL: U24703; BAB91599.1; ..
 CC CC EMBL: D63520; BAA09788.1; ALT_INIT.
 CC CC EMBL: AK017094; BAB30592.1; ..
 CC CC MGD: MG1103322; Reelin.
 CC CC GO: GO:0007420; P:brain development; IMP.
 CC CC GO: GO:0016477; P:cell migration; IMP.
 CC CC InterPro: IPR006209; EGF like.
 CC CC InterPro: IPR002860; GH BNR.
 CC CC InterPro: IPR005210; IEGF.
 CC CC InterPro: IPR002851; Reeler.
 CC CC Pfam: PF02012; BNR; 15.
 CC CC Pfam: PF00008; EGF; 5.
 CC CC Pfam: PF02014; Reeler; 1.
 CC CC SMART: SM00181; EGF; 5.
 CC CC PROSITE: PS00022; EGF_1; 7.
 CC CC PROSITE: PS01196; EGF_2; 6.
 CC CC Hydrolase: Serine protease; Developmental protein; Matrix protein;
 CC CC Cell adhesion; EGF-like domain; Glycoprotein; Repeat; Signal;
 CC CC Alternative splicing.
 CC CC SIGNAL 1 26
 CC CC CHAIN 27 3461 POTENTIAL.
 CC CC DOMAIN 40 172 REELIN.
 CC CC DOMAIN 671 702 REELER.
 CC CC DOMAIN 1030 1061 EGF-LIKE 1.
 CC CC DOMAIN 1409 1442 EGF-LIKE 2.
 CC CC DOMAIN 1765 1796 EGF-LIKE 3.
 CC CC DOMAIN 2129 2161 EGF-LIKE 4.
 CC CC DOMAIN 2478 2509 EGF-LIKE 5.
 CC CC DOMAIN 2553 2884 EGF-LIKE 6.
 CC CC DOMAIN 2853 2884 EGF-LIKE 7.

FT DOMAIN 3228 3260 EGF-LIKE 8.
 FT REPEAT 593 604 BNR 1.
 FT REPEAT 799 810 BNR 2.
 FT REPEAT 952 963 BNR 3.
 FT REPEAT 1157 1168 BNR 4.
 Query Match 52.3%; Score 46; DB 1; Length 3461;
 Best Local Similarity 71.4%; Pred. No. 37;
 Matches 10; Conservative 0; Mismatches 2; Indels 2; Gaps 1;
 QY 3 YPSNGCGLY--YSS 14
 DR 1974 YPGNGGLKPYSS 1987
 RESULT 6
 REELIN_RAT
 ID REELIN_RAT STANDARD; PRT: 3462 AA.
 AC PS8751;
 DT 28-FEB-2003 (Rel. 41, Created;
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DE 28-FEB-2003 (Rel. 41, Last annotation update)
 GN Reelin precursor (EC 3.4.21.-).
 OS Rattus norvegicus (Rat).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 CC NCBI_TaxID=10116;
 RN REELIN.
 RP SEQUENCE FROM N.A. (ISOFORM 1).
 RC TISSUE=Cerebellum;
 RA Kikkawa S., Terashima T.;
 RL Submitted (SEP-2000) to the EMBL/GenBank/DBSC databases.
 RN [2]
 RP ALTERNATIVE SPLICING.
 RX MEDLINE=99263416; PubMed=10328932;
 RA Labrest de Courvoit C., Bernier B., Royaux I., de Bergeyck V.,
 RA Goffinet A.M.;
 RT "Evolutionarily conserved, alternative splicing of reelin during brain
 CC development.";
 RL Exp. Neurol. 156:229-238(1999).
 CC -!- FUNCTION: Extracellular matrix serine protease that plays a role
 CC in layering of neurons in the cerebral cortex and cerebellum.
 CC Regulates microtubule function in neurons and neuronal migration.
 CC Affects migration of sympathetic preganglionic neurons in the
 CC spinal cord, where it seems to act as a barrier to neuronal
 CC migration. Enzymatic activity is important for the modulation of
 CC cell adhesion. Binding to the extracellular domains of lipoprotein
 CC receptors VLDLR and ApoER2 induces tyrosine phosphorylation of
 CC Dab1 and modulation of tau phosphorylation (By similarity).
 CC -!- SUBUNIT: Binds to the ectodomains of VLDLR and ApoER2 (By
 CC similarity).
 CC -!- SUBCELLULAR LOCATION: Secreted (By similarity).
 CC -!- ALTERNATIVE PRODUCTS:
 CC Event=Alternative splicing; Named isoforms=3;
 CC Name=1;
 CC IsoId=PS8751-1; Sequence=Displayed;
 CC Name=2;
 CC IsoId=PS8751-2; Sequence=VSP_005579;
 CC Name=3;
 CC IsoId=PS8751-3; Sequence=VSP_005580;
 CC -!- TISSUE SPECIFICITY: Abundantly produced during brain ontogenesis
 CC by the Cajal-Retzius cells and other pioneer neurons located in
 CC the telencephalic marginal zone and by granule cells of the
 CC external granular layer of the cerebellum.
 CC -!- DOMAIN: The basic C-terminal region is essential for secretion (By
 CC similarity).
 CC -!- SIMILARITY: BELONGS TO THE REELIN FAMILY.
 CC -!- SIMILARITY: Contains 8 EGF-like domains.
 CC -!- SIMILARITY: Contains 15 BNR repeats.
 CC -----
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 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -

CC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RE SEQUENCE FROM N.A., AND TISSUE SPECIFICITY.
 RC TISSUE=Testis;
 RX PubMed=12029070;
 RA Miyagawa Y., Tanaka H., Iguchi N., Kitamura K., Nakamura Y.,
 RA Takanashi T., Matsumiya K., Okuyama A., Nishimune Y.,
 RT "Molecular cloning and characterization of the human orthologue of
 RL male germ cell-specific actin capping protein alpha3 (capalpha3).";
 RL Mol. Hum. Reprod. 8:531-539(2002).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Testis;
 RA Kawakami B., Sugiyama A., Takemoto M., Suzuki Y., Hata H.,
 RA Nakagawa K., Mizuno S., Morinaga M., Kawamura M., Sugiyama T.,
 RA Irie R., Otsuki T., Sato H., Nishikawa T., Nagai K., Isogai T.,
 RA Sugano S.,
 RT "NEDO human cDNA sequencing project.";
 RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Testis;
 RX MEDLINE=22388257; PubMed=12477932;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner J., Shenmen C.V., Schuler G.D.,
 RA Altshul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Matsumura K., Farmer A.R., Rubin G.M., Hong J.,
 RA Stapleton M., Soares M.B., Bonaldo A.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Udén T.B., Tchiviyuk S., Carninci P., Kravetz S.,
 RA Raha S., Lottner N.A., Peters G.J., Abramson R.D., Mullen S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Guraratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.R., Hulyk S.W.,
 RA Vialar D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahy J., Heltzer E., Ketterman M., Madan A.C., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shcherbakov Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Jackson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M., Skalska J., Smalios D.E.,
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.,
 RT "Generation and initial analysis of more than 15,000 full-length
 human and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 CC [1-] FUNCTION: F-ACTIN CAPPING PROTEINS BIND IN A CA(2+)-INDEPENDENT
 CC MANNER TO THE FAST GROWING ENDS OF ACTIN FILAMENTS (BARBED END);
 CC THEREBY BLOCKING THE EXCHANGE OF SUBUNIT'S AT THESE ENDS. UNLIKE
 CC OTHER CAPPING PROTEINS (SUCH AS GELSOLIN AND SEVERIN), THESE
 CC PROTEINS DO NOT SEVER ACTIN FILAMENTS. MAY PLAY A ROLE IN THE
 CC MORPHOGENESIS OF SPERMATID (BY SIMILARITY).
 CC [1-] SUBUNIT: HETERODIMER OF AN ALPHA AND A BETA SUBUNIT (BY
 CC SIMILARITY).
 CC [1-] TISSUE SPECIFICITY: Expressed exclusively in testis and sperm.
 CC Highest expression is found in the neck region of ejaculated sperm
 CC with lower levels found in the tail and postacrosome region.
 CC [1-] SIMILARITY: BELONGS TO THE F-ACTIN CAPPING PROTEIN ALPHA SUBUNIT
 CC FAMILY.
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 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL; AB053259; BAB16501.1;
 DR EMBL; AK058174; BAB17103.1;
 DR EMBL; BC016745; BAB16745.1;
 DR InterPro; IPR002189; F-actin_cap_A.
 DR Pfam; PF01267; F-actin_cap_A.1;
 DR PRINTS; PR00191; F-actinCAPA.
 DR ProDom; PD006960; F-actin_cap_A.1.

DR PROSITE; PS00748; F-ACTIN_CAPPING_A.1; FALSE_NEG.
 DR PROSITE; PS00749; F-ACTIN_CAPPING_A.2; 1.
 KW Actin-binding; Capping protein; Multigene family.
 FT CONFLICT 95 D->Y (IN REF. 3).
 SQ SEQUENCE 299 AA; 35024 MW; CEE130C8F7397F67 CRC64;
 Query Match 48.98; Score 43; DB 1; Length 299;
 Best Local Similarity 60.38; Pred. No. 9.3;
 Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
 QY 1 DRYPSGNCGL 10
 |||||
 DC 131 DHPKGNKNCNM 140
 RESJ: 9
 CAZ3_M0CJSE STANDARD; PRT; 299 AA.
 AC P70190; 09D4N3;
 CT 16-OCT-2001 (Rel. 40, Created)
 CT 16-OCT-2001 (Rel. 40, Last sequence update)
 CT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE F-actin capping protein alpha-3 subunit (CapZ alpha-3) (Germ cell-
 DE specific protein 3).
 OS Mus musculus (Mouse).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
 CX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Testis;
 RX MEDLINE=95046372; PubMed=757958;
 RA Tanaka H., Yoshimura Y., Nishina Y., Nozaki M., Nojima H.,
 RA Nishimune Y.,
 RT "Isolation and characterization of cDNA clones specifically expressed
 RT in testicular germ cells.";
 RL FEBS Lett. 355:4-10(1994).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=129/SV;
 RX PubMed=10524250;
 RA Yoshimura Y., Tanaka H., Nozaki M., Yomogida K., Shimamura K.,
 RA Yasunaga T., Nishimune Y.,
 RT "Genomic analysis of male germ cell-specific actin capping protein
 RT alpha.";
 RL Gene 237:193-199(1999).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Testis;
 RX PubMed=12466851;
 RA Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,
 RA Nikaide I., Osato N., Saito R., Suzuki H., Yamana I., Kiyosawa H.,
 RA Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gojohori T.,
 RA Badarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,
 RA Schriml L.M., Kanapin A., Matsuda H., Batalov S., Beisel K.W.,
 RA Blake E.A., Bradt D., Brusic V., Chochia C., Corbani L.E., Cousins S.,
 RA Dalla E., Dragani T.A., Fletcher C.F., Forrest A., Frazer K.S.,
 RA Gasterland T., Gariboldi M., Gissi C., Godzik A., Gough J.,
 RA Grimmond S., Gustincich S., Hirokawa N., Jackson J.J., Jarvis E.D.,
 RA Kanai A., Kawaji H., Kawasawa Y., Kedzierski R.M., King B.L.,
 RA Konagaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,
 RA Madgett D.P., Maltais L., Marchionni L., McKenzie L., Miki H.,
 RA Nagashima T., Numata K., Okido T., Pavan W.J., Pertea G., Pesole G.,
 RA Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramachandran S.,
 RA Ravasi T., Reed D.J., Reid J., Ring B.Z., Ringwald M.,
 RA Sadelin A., Schneider C., Semple C.A., Setou M., Shimada K.,
 RA Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita Y.,
 RA Verardo R., Wagner L., Warlestedt C., Wang Y., Watanabe Y., Wells C.,
 RA Wilming L.G., Wysshaw-Boris A., Yanagisawa M., Yang I., Yang L.,
 RA Yuan Z., Zavolan M., Zhu Y., Zimmer A., Carninci P., Hayatsu N.,
 RA Hirozane-Kishikawa T., Konro H., Nakamura M., Sakazume N., Sato K.,
 RA Shiraki T., Waki K., Kawai J., Aizawa K., Arakawa T., Fukuda S.,

RA Hara A., Hashizume W., Imotani K., Ishii Y., Itoh M., Kagawa I.,
RA Miyazaki A., Sakai K., Sasaki D., Shibata K., Shinagawa A.,
RA Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers C.,
RA Birney E., Hayashizaki Y.,
RT Analysis of the mouse transcriptome based on functional annotation of
RL 60,770 full-length cDNAs.",
RL Nature 420:563-573(2002).
RN [4]
RP SEQUENCE FROM N.A.
RC TISSUE=Testicle;
RX MEDLINE=22388257; PubMed=12477932;
RA Krausberg R.B., Feigold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Sherman C.M., Schuler G.D.,
RA Aitschul S.F., Ziesler B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Ksieh F.,
RA Diachenko L., Marusina K., Farmer A.A., Rubin G.N., Hong L.,
RA Stapleton M., Soares X.B., Bonaldo X.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carrincci P., Prange C.,
RA Raha S., Loquellano N.A., Peters G.G., Abramson R.D., Mullan S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.G., Malek J.A., Gunaratne P.H.,
RA Richards S., Morley K.C., Hale S., Garcia A.M., Gay L.C., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Vadan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalhus D.E.,
RA Schnerch A., Schein J.E., Jones S.C.M., Marra M.A.,
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences".
RL Proc Natl Acad Sci U.S.A. 99:16899-16903(2002).
CC -!- FUNCTION: F-ACTIN CAPPING PROTEINS BIND IN A CA(2+)-INDEPENDENT
MANNER TO THE FAST GROWING ENDS OF ACTIN FILAMENTS (BARBED END)
THEREBY BLOCKING THE EXCHANGE OF SUBUNITS AT THESE ENDS. UNLIKE
OTHER CAPPING PROTEINS (SUCH AS GELSOLIN AND SEVERIN), THESE
PROTEINS DO NOT SEVER ACTIN FILAMENTS. MAY PLAY A ROLE IN THE
MORPHOGENESIS OF SPERMATID.
CC -!- SUBUNIT: HETERODIMER OF AN ALPHA AND A BETA SUBUNIT (BY
SIMILARITY).
CC -!- TISSUE SPECIFICITY: Exclusively expressed in the testis.
CC -!- DEVELOPMENTAL STAGE: EXPRESSED IN 24-DAY-OLD AND ADULT TESTIS, BUT
NOT IN 4-, 10- AND 16-DAY-OLD TESTIS.
CC -!- SIMILARITY: BELONGS TO THE F-ACTIN CAPPING PROTEIN ALPHA SUBUNIT
FAMILY.
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DR ENBL; D87471; BAA13409.1; -
DR ENBL; AB026984; BAA81887.1; -
DR ENBL; AK016391; BAB30213.1; -
DR ENBL; BCC49620; AAY49620.1; -
DR MGD; XGI:106221; Gappa3.
DR InterPro; IPR002189; F-actin_cap_A.
DR Pfam; PF01267; F-actin_cap_A; 1.
DR PRINTS; PR00191; FACTINCAPA.
DR ProDom; PD006960; F-actin_cap_A; 1.
DR PROSITE; PS00748; F-ACTIN_CAPPING_A_1; FALSE_NEG.
DR PROSITE; PS00749; F-ACTIN_CAPPING_A_2; 1.
DR PROSITE; PS00749; F-ACTIN_CAPPING_A_2; 1.
KW Actin-binding; Capping protein; Multigene family.
FT CONFLICT 117 L -> I (IN REF. 3).
FT CONFLICT 225 F -> Y (IN REF. 3).
SQ SEQUENCE 299 AA; 34952 MW; 8C87579313F233C6 CRC64;
Query Match 48.9%; Score 43; DB 1; Length 299;
Best Local Similarity 60.0%; Pred. No. 9.3;
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 DRYPSGNCGL 10
DB 131 DHVPNGNCNV 140
RESULT 10
CAZ3 RAT STANDARD; PRT; 299 AA.
AC Q3KJY6;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE F-actin capping protein alpha-3 subunit (Capz alpha-3).
GN CAPZ3.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Testis;
RX MEDLINE=98069272; PubMed=9406198;
RA Hurst S., Howes E.A., Coadwell J., Jones R.,
RT "Expression of a testis-specific putative actin-capping protein
associated with the developing acrosome during rat spermiogenesis".
RL Mol. Reprod. Dev. 49:81-91(1998).
CC -!- FUNCTION: F-ACTIN CAPPING PROTEINS BIND IN A CA(2+)-INDEPENDENT
MANNER TO THE FAST GROWING ENDS OF ACTIN FILAMENTS (BARBED END)
THEREBY BLOCKING THE EXCHANGE OF SUBUNITS AT THESE ENDS. UNLIKE
OTHER CAPPING PROTEINS (SUCH AS GELSOLIN AND SEVERIN), THESE
PROTEINS DO NOT SEVER ACTIN FILAMENTS. MAY PLAY A ROLE IN THE
MORPHOGENESIS OF SPERMATID.
CC -!- SUBUNIT: HETERODIMER OF AN ALPHA AND A BETA SUBUNIT (BY
SIMILARITY).
CC -!- TISSUE SPECIFICITY: Exclusively expressed in the testis.
CC -!- SIMILARITY: BELONGS TO THE F-ACTIN CAPPING PROTEIN ALPHA SUBUNIT
FAMILY.
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DR ENBL; Y12538; CAA3137.1; -
DR InterPro; IPR002189; F-actin_cap_A.
DR Pfam; PF01267; F-actin_cap_A; 1.
DR PRINTS; PR00191; FACTINCAPA.
DR ProDom; PD006960; F-actin_cap_A; 1.
DR PROSITE; PS00748; F-ACTIN_CAPPING_A_1; FALSE_NEG.
DR PROSITE; PS00749; F-ACTIN_CAPPING_A_2; 1.
KW Actin-binding; Capping protein; Multigene family.
SQ SEQUENCE 299 AA; 35007 MW; 3D753088BCF799E5 CRC64;
Query Match 48.9%; Score 43; DB 1; Length 299;
Best Local Similarity 60.0%; Pred. No. 9.3;
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 DRYPSGNCGL 10
DB 131 DHVPNGNCNV 140
RESULT 11
CH9 LYNDI STANDARD; PRT; 121 AA.
ID CH9A LYNDI
AC P50603;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 01-OCT-1996 (Rel. 34, Last annotation update)
DE Chorion class A proteins LD9 (Fragment).
DE

OS Lymantria dispar (Gypsy moth).
 CC Eukaryota; Metazoa; Arthropoda; Insecta; Pterygota;
 CC Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia; Noctuoidea;
 CC Lymantriidae; Lymantria.
 CX NCBI_TaxID=11123;
 RN [-]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Choriogenic follicles;
 RX MEDLINE=95018300; PubMed=7932786;
 RA Leclerc R.F., Regier J.C.;
 RT "Evolution of chorion gene families in lepidoptera: characterization
 RT of 15 cDNAs from the Gypsy moth";
 RL J. Mol. Evol. 39:244-254(1994).
 CC -!- FUNCTION: THIS PROTEIN IS ONE OF MANY FROM THE EGGSHELL OF THE
 CC GYPSY MOTH.
 CC -!- SIMILARITY: MEMBER OF THE ALPHA-BRANCH OF CHORION PROTEIN TO WHICH
 CC BELONG CLASSES A, CA AND HCA.
 CC -----
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 CC -----
 DR EMBL; J04661; A0467861.1; -;
 KW Eggshell; Chorion; Repeat; Multigene family.
 FT NON TER 1
 SQ SEQUENCE 121 AA; 11617 MW; 528E28501ED56617 CRC64;
 Query Match 46.6%; Score 41; DB 1; Length 121;
 Best Local Similarity 66.7%; Pred. No. 7.8;
 Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
 QY 2 RYPSGNCL 10
 DB 4: RYPGACGI 43
 RESULT 12
 YK78_AERPE STANDARD; PRT; 437 AA.
 ID YK78_AERPE
 AC Q9YA60;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Hypothetical protein APE2078.
 GN APE2078.
 OS Aeropyrum pernix.
 CC Archaea; Crenarchaeota; Thermoprotei; Desulfurococcales;
 CC Desulfurococaceae; Aeropyrum.
 CX NCBI_TaxID=56636;
 RN [-]
 RP SEQUENCE FROM N.A.
 RC STRAIN=K1.
 RX MEDLINE=99310339; PubMed=10382966;
 RA Kawarabayashi Y., Hino Y., Horikawa H., Yamazaki S., Haikawa Y.,
 RA Jin-no K., Takahashi M., Sekine N., Baba S.-I., Arkai A., Kcsugi H.,
 RA Hcsayama A., Fukui S., Nagai Y., Nishijira K., Nakazawa H.,
 RA Takamiya M., Masuda S., Funahashi T., Tanaka T., Kudoh Y.,
 RA Yamazaki J., Kishida N., Oguchi A., Aoki K.-I., Kubota K.,
 RA Nakamura Y., Nomura N., Sato Y., Kikuchi H.,
 RT "Complete genome sequence of an aerobic hyper-thermophilic
 RT crenarchaeon, Aeropyrum pernix K1";
 RL DNA Res. 6:183-101(1999).
 CC -!- SIMILARITY: Belongs to the ubiD family.
 CC -----
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 CC -----
 DR EMBL; AP000363; BAA81089.1; -;
 DR PIR; A72513; A72513.
 DR InterPro; IPR002830; carboxylase.
 DR Pfam; PF01977; UbiD; 1.
 DR TIGRFAMs; TIGR00148; TIGR00148; 1.
 KW Hypothetical protein; Complete proteome.
 SQ SEQUENCE 437 AA; 47635 MW; 5055140A80A2D602 CRC64;
 Query Match 46.6%; Score 41; DB 1; Length 437;
 Best Local Similarity 57.1%; Pred. No. 29;
 Matches 8; Conservative 1; Mismatches 5; Indels 0; Gaps 0;
 QY 2 RYPSGNCLYSSG 15
 DB 112 RYVEGEAGLYSSG 25
 RESULT 13
 CTA0_HUMAN STANDARD; PRT; 488 AA.
 ID CTA0_HUMAN
 AC Q9GNM4; Q96C9; Q950N5;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Protein C20orf100.
 GN C20orf100.
 OS Homo sapiens (Human).
 CC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 CX NCBI_TaxID=9606;
 RN [-]
 RP SEQUENCE FROM N.A. (ISOFORM 1).
 RC TISSUE=Brain;
 RA Suzuki O., Sasaki N., Aotsuka S., Shoji T., Ichihara T., Shiohata N.,
 RA Matsumoto K., Hirano M., Sano S., Nomura R., Yoshikawa Y.,
 RA Matsumura Y., Moriya S., Chiba E., Morioka H., Chogawa S.,
 RA Kasriyama S., Satoh N., Matsunawa H., Takahashi E., Kataoka R.,
 RA Kuga K., Kuroda A., Satoh I., Kamata K., Otsuki T., Sato H., Ota T.,
 RA Watanabe Y., Sugiyama T., Irie R., Otsuki T., Sato H., Ota T.,
 RA Nishikawa T., Kimura K., Yamashita H., Matsuo K., Nakamura Y.,
 RA Sekine M., Kikuchi H., Kanda K., Wagatsuna M., Murakawa K.,
 RA Kanehori K., Takahashi-Fujii A., Oshima A., Sugiyama A., Kawakami B.,
 RA Suzuki Y., Sugano S., Nagahari K., Masuho Y., Nagai K., Isogai T.;
 RT "NEO human cDNA sequencing project";
 RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
 RN [-]
 RP SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).
 RX MEDLINE=21638749; PubMed=11780052;
 RA Deloukas P., Matthews L.H., Ashurst J., Burton J., Gilbert J.G.R.,
 RA Jones X., Stavrides G., Alreida J.P., Babbage A.K., Bagguley C.L.,
 RA Bailey J., Barlow K.F., Bates K.N., Beard L.M., Beare D.M., Brown A.J.,
 RA Beasley O.P., Bird C.P., Blakey S.E., Bridgeman A.M., Brown A.J.,
 RA Buck D., Burrill W.D., Butler A.P., Carder C., Carter N.P.,
 RA Chapman J.C., Clamp M., Clark G., Clark L.N., Clark S.Y., Clee C.M.,
 RA Clegg S., Cobley V.E., Collier R.E., Connor R.E., Corby N.R.,
 RA Coulson A., Coville G.J., Deadman R., Dhani P.D., Dunn M.,
 RA Ellington A.G., Frankland J.A., Fraser A., French L., Garner P.,
 RA Grahame D.V., Griffiths C., Griffiths M.N.D., Gwilliam R., Hall R.E.,
 RA Hammond S., Harley J.L., Heath P.D., Ho S., Holden J.L., Howden P.J.,
 RA Huckle E., Hunt A.R., Hunt S.E., Jekosch K., Johnson C.M., Johnson D.,
 RA Kay M.P., Kimberley A.M., King A., Knights A., Laird G.K., Lawlor S.,
 RA Leharvalho M.H., Leverhwa M.A., Lloyd C., Lloyd D.M., Lovell J.D.,
 RA Marsh V.L., Martin S.L., McConachie L.J., McLeay K., McMurray A.A.,
 RA Milne S.A., Mistry D., Moore M.J.F., Mullikin J.C., Nickerson T.,
 RA Oliver K., Parker A., Patel R., Pearce T.A.V., Peck A.I.,
 RA Phillimore B.J.C., Prichard S.R., Plumb R.W., Ramsay H.,
 RA Rice C.M., Ross M.T., Scott C.E., Sehra H.K., Showkeen R., Sims S.,
 RA Skuce C.D., Smith M.L., Soderlund C., Steward C.A., Sulston C.E.,
 RA Swann R.M., Sycamore N., Taylor R., Tee L., Thomas D.W., Thorpe A.,

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RA Tracey A., Tromans A.C., Vaudin M., Wall M.L., Wallis J.M.,
RA Whitehead S.L., Whitaker P., Willey D.L., Williams S.A.,
RA Wilming L., Wray P.W., Hubbard T., Curbin R.M., Bentley D.R., Beck S.,
RA Rogers J.;
BT "The DNA sequence and comparative analysis of human chromosome 20.";
EL Nature 414:865-871(2001);
EN (1);
RP SEQUENCE FROM N.A. (ISOFORM 2);
KC TISSUE=Muscle;
RX MEDLINE=22388257; PubMed=12477332;
RA Strausberg R.L., Feilboid E.A., Grouse L.H., Derge J.S.,
RA Klausner R.D., Collins F.S., Wagner L., Shennan C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buckow K.H., Schaefer C.F., Brat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Dlatchenko L., Marusira K., Farber A.A., Rubin G.M., Horg L.,
RA Stapleton M., Soares M.B., Borraldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.C., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Kalex C.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
RA Whitting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzyzinski M., Skalska J., Smalios D.E.,
RA Schnerch A., Schein J.E., Jones S.C.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length
RT human and mouse cDNA sequences.";
PL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
CC -1- ALTERNATIVE PRODUCTS;
CC Event=Alternative splicing; Named isoforms=2;
CC Name=1;
CC Name=2;
CC IsoId=Q96NM4-1; Sequence=Displayed;
CC Note=Q96NM4-2; Sequence=VSP_002187;
CC Note=No experimental confirmation available;
CC -1- SIMILARITY: Contains 1 HMG box domain;
CC -1- CAUTION: It is uncertain whether Met-1 or Met-52 is the initiator.
CC -1- CAUTION: Ref.1 (CAC36288) sequence differs from that shown due to
CC erroneous gene model prediction.
CC -----
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CC -----
CC EMBL: AK055135; BA070860.1; -
CC EXBL: AL034419; CAD43476.1; -
CC EXBL: AL034419; CAD43477.1; -
CC EXBL: AL121987; CAC36288.1; ALT_SEQ.
CC EXBL: BC007636; AAH07636.1; -
CC Genew: HGNC:16095; C2Cort100.
CC InterPro: IPR000910; HMG_12_box.
CC Pfam: PF00505; HMG_box; 1
CC PROSITE: PS01118; HMG_BOX_2; 1
CC Nuclear protein; DNA-Binding; Alternative splicing.
FT DNA_BIND 255 323 HMG_BOX.
FT DOMAIN 245 250 POLY-LYS.
FT DOMAIN 372 456 PRO-RICH.
FT VARSPLIC 302 302 Q -> CAYKRKTEAKKEY;KALAAVRSLSVK (in
FT isoform 2).
FT FTId=VSP_002187.
FT CONFLICT 482 482 D -> N (ZIN REF. 1).
SQ SEQUENCE 488 AA; 51604 MW; 687FD144CF30731A CRC64;
Query Match 46.8%; Score 41; DB 1; Length 488;
Best Local Similarity 75.0%; Pred. No. 32;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
```

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Cy 3 YPSGNCGL 10
Db 466 YPSGECGI 473
RESULT 14
DNB2_ADEC7
ID DNB2_ADEC7 STANDARD; PRT; 517 AA.
AC P04497;
DT 13-AUG-1987 (Rel. 05, Created)
DT 13-AUG-1987 (Rel. 05, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
GB Early E2A DNA-binding protein.
OS Human adenovirus type 7.
CC Viruses; dsDNA viruses, no RNA stage; Adenoviridae; Mastadenovirus.
CX NCBI_TaxID=10519;
RN (1)
RP SEQUENCE FROM N.A.
RX MEDLINE=84185604; PubMed=6325415;
RA Quinn C.O., Kitchingman G.R.;
RT "Sequence of the DNA-binding protein gene of a human subgroup B
RT adenovirus (type 7). Comparisons with subgroup C (type 5) and
RT subgroup A (type 12).";
RL C. Sol. Chem. 259:5003-5009(1984).
CC -1- FUNCTION: BINDS COOPERATIVELY SINGLE-STRANDED DNA IN A SEQUENCE-
CC INDEPENDENT MANNER. INVOLVED IN DNA-REPLICATION. REGULATION OF
CC MRNA FORMATION, AND HOST-RANGE SPECIFICITY. ZINC IS REQUIRED
CC FOR DNA BINDING.
CC -1- SUBCELLULAR LOCATION: NUCLEAR. ACCUMULATES IN INFECTED CELLS.
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL: K02530; AAA42508.1; -
CC PIR: A03834; ERA0A7.
CC HSPSP; P03265; IADU.
CC InterPro: IPR003176; Vir_DNA_binding.
CC InterPro: IPR005376; Vir_DNA_Zn_bind.
CC Pfam: PF02236; Vir_DNA_binding; 1.
CC Pfam: PF07728; Vir_DNA_Zn_bind; 2.
CC Early protein; DNA-binding; Zinc-finger; Phosphorylation;
CC Nuclear protein.
FT MOD_RES 180 190 PHOSPHORYLATION (PROBABLE).
FT ZN_FING 258 271 POTENTIAL.
SQ SEQUENCE 517 AA; 58306 MW; A2CC8B1C4A1F191F CRC64;
Query Match 46.8%; Score 41; DB 1; Length 517;
Best Local Similarity 33.3%; Pred. No. 34;
Matches 5; Conservative 7; Mismatches 3; Indels 0; Gaps 0;
Cy 1 DRYPSGNCGLYSSG 15
Db 333 NQFSSKSCGMFYTEG 347
RESULT 15
VP02_BPFRD
ID VP02_BPFRD STANDARD; PRT; 590 AA.
AC P27378;
DT 01-AUG-1992 (Rel. 23, Created)
DT 01-DEC-1992 (Rel. 24, Last sequence update)
DT 01-DEC-1992 (Rel. 24, Last annotation update)
DE Adsorption protein P2.
GN I1.
OS Bacteriophage PRD1.
CC Viruses; dsDNA viruses, no RNA stage; Tectiviridae; Tectivirus.
CX NCBI_TaxID=10658;
```

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RN [1]
RP SEQUENCE FROM N.A. AND SEQUENCE OF 1-9.
RX MEDLINE=91306449; PubMed=1853567;
RA Bamford J.K.H., Haenninen A.-L., Pakula T.M., Ojala P.M.,
RA Kalkkinen N., Frilander M., Bamford D.R.;
RT "Genome organization of membrane-containing bacteriophage PRD1.";
RL Virology 183:658-676(1991).
CC -1- FUNCTION: THE LIFE CYCLE OF THE PHAGE BEGINS WHEN THE PHAGE
CC ADSORBS TO ITS RECEPTOR ON THE SURFACE OF THE HOST VIA THE
CC ADSORPTION PROTEIN P2 AND INJECTS ITS DNA INTO THE HOST CYTOPLASM.
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; M69077; AAA32458.1; -
DR PIR; D40477; WMBPQ2. 0
FT INIT MET
SQ SEQUENCE 590 AA; 63690 MW; 5ACA024C92B8F6RC CRC64;

Query Match 45.6%; Score 41; DB 1; Length 590;
Best Local Similarity 46.7%; Pred. No. 39;
Matches 7; Conservative 3; Mismatches 5; Indels 2; Gaps 2;

QY 1 DRYPSGNCGLYSSG 15
| : : : : :
DB 407 DEWYANKGLFPMSG 421
```

Search completed: November 5, 2003, 16:46:21
Job time : 2.66079 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 5, 2003, 16:37:23 ; Search time 1.92336 Seconds
(without alignments)
1952.598 Million cell updates/sec

Title: US-09-902-563-18
Perfect score: 88
Sequence: 1 DRYPSGNCGLYSSG 15

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 830525 seqs, 258052604 residues

Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database: SPTREMBL_23.*
1: sp_archaea.*
2: sp_bacteria.*
3: sp_fungi.*
4: sp_human.*
5: sp_invertebrate.*
6: sp_mammal.*
7: sp_mhc.*
8: sp_organelle.*
9: sp_phase.*
10: sp_plant.*
11: sp_ricent.*
12: sp_virus.*
13: sp_vertebrate.*
14: sp_unclassified.*
15: sp_virus.*
16: sp_bacteria.*
17: sp_archaea.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Result No.	Score	Match	Length	DB ID	Description
1	88	100.0	357	12 Q9EPT7	Q9EPT7 rattus norv
2	88	100.0	442	6 Q8VIP7	Q8VIP7 sus scrofa
3	56	63.6	220	5 Q878A2	Q878A2 ciona savig
4	56	63.6	652	5 Q9NQJ1	Q9NQJ1 ciona intes
5	46	52.3	1785	4 Q9V2L1	Q9V2L1 homo sapien
6	46	52.3	1785	4 Q9V4V9	Q9V4V9 homo sapien
7	46	52.3	2403	4 Q9UGV2	Q9UGV2 homo sapien
8	46	52.3	2412	4 Q9UJ57	Q9UJ57 homo sapien
9	46	52.3	2413	4 Q9GDU4	Q9GDU4 homo sapien
10	46	52.3	2413	4 Q9UKJ4	Q9UKJ4 homo sapien
11	46	52.3	2426	4 Q9UGV3	Q9UGV3 homo sapien
12	45	51.1	183	4 Q8TAE0	Q8TAE0 homo sapien
13	45	51.1	210	4 Q8NBS2	Q8NBS2 homo sapien
14	45	51.1	210	4 Q8TAC6	Q8TAC6 homo sapien
15	44.5	50.6	457	11 Q8R0Z6	Q8R0Z6 mus musculu
16	44	50.0	217	7 Q9GJH7	Q9GJH7 salmo trutt

SUMMARIES

Query Match 100.0%; Score 88; DB 11; Length 357;
Best Local Similarity 100.0%; Pred. No. 2.1e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DRYPSGNCGLYSSG 15
|||||
DB 282 DRYPSGNCGLYSSG 296

RESULT 2
Q8MIP7 PRELIMINARY; PRT: 442 AA.
ID Q8MIP7
AC Q8MIP7;

ALIGNMENTS

Q9EPT7 PRELIMINARY; PRT: 357 AA.
AC Q9EPT7;
DT 01-MAR-2001 (TREMBLrel. 16, Created;
DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE Prothrombinase FGU2.
CS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
CX NCBI_TaxID=10116;
RY [1]
RZ SEQUENCE FROM N.A.
RC STRAIN=Sprague-Dawley;
RA Rychnik D.F., Chien E., Philippe M.;
RT "FGL2 Expression in the Sprague-Dawley Rat."
RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF123608; AAC42269.1; --
DR HSSP: PC2671; 1PZD.
DR InterPro: IPR002181; Fibrinogen_C.
DR Pfam: PF0C147; fibrinogen_C; 1.
DR SMART: SM00186; FBG; 1.
DR PROSITE: PS00514; FIBRIN_AG_C-PCMAIN; 1.
SQ SEQUENCE 357 AA; 40966 MW; 31193DD9A02EBBA9 CRC64;

DT 01-OCT-2002 (TrEMBLrel. 22, Created)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
 DE Fibrinogen-like protein 2.
 GN FGL2.
 OS Sus scrofa (Pig).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
 OX NCBI_TaxID=9923;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Ghanekar A., Liu H., Grant D.R., Levy G.A.;
 RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AY112657; AAM52324.1; -
 DR InterPro: IPR002181; Fibrinogen_C.
 DR Pfam: PF00147; Fibrinogen_C.1.
 DR SMART: SM00186; FBG; 1.
 DR PROSITE: PS00514; FIBRIN_AG_C_DOMAIN; 1.
 SQ SEQUENCE 442 AA; 50579 MW; 67800D67AEDFF899 CRC64;

Query Match 100.0%; Score 88; DB 6; Length 442;
 Best Local Similarity 100.0%; Pred. No. 2.6e-06;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DRYPSGNCGLYSSG 15
 |||||.....
 DB 367 DRYPSGNCGLYSSG 381

RESULT 3

Q8T8A2
 AC Q8T8A2 PRELIMINARY; PRT; 220 AA.
 DT 01-JUN-2002 (TrEMBLrel. 21, Created)
 DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
 DE Fibrinogen-like protein (fragment).
 GN CS-FIBRINOGEN-LIKE.
 OS Ciona savignyi.
 OC Eukaryota; Metazoa; Chordata; Urochordata; Ascidiacea; Enterogona;
 OC Phlebobranchia; Cionidae; Ciona.
 OX NCBI_TaxID=51511;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA MEDLINE=21920613; Pubmed=11923298;
 RA Imai K.S., Satoh N., Satou Y.;
 RT "Early embryonic expression of RGF4/6/9 gene and its role in the
 induction of mesenchyme and notochord in Ciona savignyi embryos."
 RL Development 129:1729-1738(2002).
 DR EMBL: AB073373; BA888674.1; -
 DR InterPro: IPR002181; Fibrinogen_C.
 DR Pfam: PF00147; fibrinogen_C.1.
 DR SMART: SM00186; FBG; 1.
 DR PROSITE: PS00514; FIBRIN_AG_C_DOMAIN; 1.
 DT NON TER
 SQ SEQUENCE 220 AA; 25758 MW; 4160FAE727F3ED06 CRC64;

Query Match 63.6%; Score 56; DB 5; Length 220;
 Best Local Similarity 66.7%; Pred. No. 0.24;
 Matches 10; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 DRYPSGNCGLYSSG 15
 |||||.....
 DB 143 DRYPSGNCGLYSSG 157

RESULT 4

Q9NDQ1
 ID Q9NDQ1 PRELIMINARY; PRT; 652 AA.
 AC Q9NDQ1
 DT 01-OCT-2000 (TrEMBLrel. 15, Created)
 DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)

DE Fibrinogen-like protein.
 GN Cl-FIBRN.
 OS Ciona intestinalis.
 OC Eukaryota; Metazoa; Chordata; Urochordata; Ascidiacea; Enterogona;
 OC Phlebobranchia; Cionidae; Ciona.
 OX NCBI_TaxID=7719;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Satoh K., Takahashi H., Asakura T., Satoh B., Takatori N., Satou Y.,
 RA Satoh N.;
 RL "Characterization of Brachyury downstream notochord genes in the Ciona
 intestinalis embryo."
 RL Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AB036849; BAB00636.1; -
 DR HSSP: P02671; IF2D.
 DR InterPro: IPR002181; Fibrinogen_C.
 DR Pfam: PF00147; fibrinogen_C.1.
 DR SMART: SM00186; FBG; 1.
 DR PROSITE: PS00514; FIBRIN_AG_C_DOMAIN; 1.
 SQ SEQUENCE 652 AA; 73252 MW; A492BA325162F0E0 CRC64;

Query Match 63.6%; Score 56; DB 5; Length 652;
 Best Local Similarity 66.7%; Pred. No. 0.73;
 Matches 10; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 DRYPSGNCGLYSSG 15
 |||||.....
 DB 574 DRYPSGNCGLYSSG 588

RESULT 5

C9Y211
 ID C9Y211 PRELIMINARY; PRT; 1785 AA.
 AC C9Y211
 DT 01-NOV-1999 (TrEMBLrel. 12, Created)
 DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
 DE DVB1.
 GN DVB1.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA MEDLINE=20017478; Pubmed=10551316;
 RA Takeshita H., Sato M., Shiwaku H.O., Samba S., Sakurada A., Hoshi M.,
 RA Hayashi Y., Igawa Y., Ayabe H., Horii A.;
 RT "Expression of the DMB1 gene is frequently suppressed in human lung
 cancer."
 RL Jpn. J. Cancer Res. 90:903-908(1999).
 CC -1- SIMILARITY: CONTAINS 2 CUB DOMAINS.
 DR EMBL: AB020851; BAA78577.1; -
 DR EMBL: AB020812; BAA78577.1; JOINED.
 DR EMBL: AB020813; BAA78577.1; JOINED.
 DR EMBL: AB020814; BAA78577.1; JOINED.
 DR EMBL: AB020815; BAA78577.1; JOINED.
 DR EMBL: AB020816; BAA78577.1; JOINED.
 DR EMBL: AB020817; BAA78577.1; JOINED.
 DR EMBL: AB020818; BAA78577.1; JOINED.
 DR EMBL: AB020819; BAA78577.1; JOINED.
 DR EMBL: AB020820; BAA78577.1; JOINED.
 DR EMBL: AB020821; BAA78577.1; JOINED.
 DR EMBL: AB020822; BAA78577.1; JOINED.
 DR EMBL: AB020823; BAA78577.1; JOINED.
 DR EMBL: AB020824; BAA78577.1; JOINED.
 DR EMBL: AB020825; BAA78577.1; JOINED.
 DR EMBL: AB020826; BAA78577.1; JOINED.
 DR EMBL: AB020827; BAA78577.1; JOINED.
 DR EMBL: AB020828; BAA78577.1; JOINED.
 DR EMBL: AB020829; BAA78577.1; JOINED.
 DR EMBL: AB020830; BAA78577.1; JOINED.
 DR EMBL: AB020831; BAA78577.1; JOINED.

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DR EMBL; AB020832; BAA78577.1; JOINED.
DR EMBL; AB020833; BAA78577.1; JOINED.
DR EMBL; AB020834; BAA78577.1; JOINED.
DR EMBL; AB020835; BAA78577.1; JOINED.
DR EMBL; AB020836; BAA78577.1; JOINED.
DR EMBL; AB020837; BAA78577.1; JOINED.
DR EMBL; AB020838; BAA78577.1; JOINED.
DR EMBL; AB020839; BAA78577.1; JOINED.
DR EMBL; AB020840; BAA78577.1; JOINED.
DR EMBL; AB020841; BAA78577.1; JOINED.
DR EMBL; AB020842; BAA78577.1; JOINED.
DR EMBL; AB020843; BAA78577.1; JOINED.
DR EMBL; AB020844; BAA78577.1; JOINED.
DR EMBL; AB020845; BAA78577.1; JOINED.
DR EMBL; AB020846; BAA78577.1; JOINED.
DR EMBL; AB020848; BAA78577.1; JOINED.
DR EMBL; AB020849; BAA78577.1; JOINED.
DR EMBL; AB020850; BAA78577.1; JOINED.
DR InterPro; IPR000859; CUB domain.
DR InterPro; IPR001507; Endoglin/CD105.
DR InterPro; IPR001190; Srcr_receptor.
DR Pfam; PF00431; CUB; 2.
DR Pfam; PF00530; SRCR; 9.
DR Pfam; PF001030; zona_pellucida; 1.
DR PRINTS; PR00258; SPERACTRCPTR.
DR SMART; SM00042; CUB; 2.
DR SMART; SM00241; ZP; 1.
DR PROSITE; PS01180; CUB; 2.
DR PROSITE; PS00420; SRCR_1; 8.
DR PROSITE; PS0287; SRCR_2; 9.
DR PROSITE; PS00682; ZP_DOMAIN; 1.
DR PROSITE; PS00682; ZP_DOMAIN; 1.
DR SIGNAL; 1 25 POTENTIAL.
DR FT CHAIN 26 1785 DMPT1/6KB.1 PROTEIN.
DR SQ SEQUENCE 1785 AA; 193941 MW; 7BIF8D47E4A82092 CRC64;

Query Match 52.3%; Score 46; DB 4; Length 1785;
Best Local Similarity 64.3%; Pred. No. 93;
Matches 9; Conservative 2; Mismatches 1; Indels 2; Gaps 1;

QY 4 P5GNCG--LYSSG 15
DB 1134 PSSNCGGFLFYASG 1147

RESULT 7
Q9UGM2 PRELIMINARY; PRT; 2403 AA.
AC Q9UGM2;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
DE DMPT1/8kb.1 protein.
GN DMPT1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN 1;
RP SEQUENCE FROM N.A.
RC TISSUE=lung; PubMed=10597221;
RX MEDLINE=20065069; PubMed=10597221;
RA Mollenhauer J., Holmskov U., Wiemann S., Krebs I., Herbertz S.,
RA Madisen J., Kioschis P., Coy J.F., Poustka A.;
RT "The genomic structure of the DMPT1 gene: evidence for a region with
RT susceptibility to genomic instability.";
EL Occurence 18:6233-6240(1999).
CC 1- SIMILARITY: CONTAINS 2 CUB DOMAINS.
EMBL; AB020824; CAB63942.1;
CC InterPro; IPR00859; CUB domain.
CC InterPro; IPR001507; Endoglin/CD105.
DR InterPro; IPR006141; Interf.
DR InterPro; IPR001190; Srcr_receptor.
DR Pfam; PF00431; CUB; 2.
DR Pfam; PF00530; SRCR; 14.
DR Pfam; PF001030; zona_pellucida; 1.
DR PRINTS; PR00258; SPERACTRCPTR.
DR SMART; SM00042; CUB; 2.
DR SMART; SM00241; ZP; 1.
DR TIGRfams; TIGR01443; interm_cterm; 13.
DR PROSITE; PS01180; CUB; 2.
DR PROSITE; PS00420; SRCR_1; 13.
DR PROSITE; PS0287; SRCR_2; 14.
DR PROSITE; PS00682; ZP_DOMAIN; 1.
DR FT CHAIN 26 2403 DMPT1/8KB.1 PROTEIN.
DR SQ SEQUENCE 2403 AA; 259573 MW; 902622DE7399AD38 CRC64;

Query Match 52.3%; Score 46; DB 4; Length 2403;
Best Local Similarity 64.3%; Pred. No. 13e+02;
Matches 9; Conservative 2; Mismatches 1; Indels 2; Gaps 1;

QY 4 P5GNCG--LYSSG 15
DB 1752 PSSNCGGFLFYASG 1765

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RA Mollerhauer J.;
RT Major subforms of DBT1 are gastrointestinal mucins that display
RT extensive alternative splicing and differential protein targeting.;
RL Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: CONTAINS 2 CUB DOMAINS.
DR EMBJ; AJ297935; CAC44122.1; -.
DR InterPro; IPR000859; CUB domain.
DR InterPro; IPR001507; Endoglin/CD105.
DR InterPro; IPR006141; Intein_receptor.
DR InterPro; IPR001190; Srcr_receptor.
DR Pfam; PF00431; CUB; 2.
DR Pfam; PF00530; SRCR; 14.
DR Pfam; PF00100; zona_pellucida; 1.
DR PRINTS; PR00258; SPERACTRCPTR.
DR SMART; SM00042; CUB; 2.
DR SMART; SM00202; SR; 14.
DR SMART; SM0241; ZP; 1.
DR TIGRfams; TIGR01443; Intein_Cterm; 13.
DR PROSITE; PS01180; CUB; 2.
DR PROSITE; PS00420; SRCR_1; 13.
DR PROSITE; PS0287; SRCR_2; 14.
DR PROSITE; PS00682; ZP_DOMAIN; 1.
KW Signal.
FT SIGNAL. 1 25 POTENTIAL.
FT CHAIN. 26 2412 DBT1/8KB.2 PROTEIN.
SQ SEQUENCE 2412 AA; 260568 MW; 3F630CCBFF18EDD CRC64;

Query Match 52.3%; Score 46; DB 4; Length 2412;
Best Local Similarity 64.3%; Pred. No. 1.3e+02;
Matches 9; Conservative 2; Mismatches 1; Indels 2; Gaps 1;

QY 4 PSNGCG--LYSSG 15
DB 1762 PSSNCGFLFVASG 1775

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Q96D04 PRELIMINARY; PRT; 2413 AA.
AC Q96D04;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
DE DBT1/8kb.2 protein precursor.
GN DBT1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RS SEQUENCE FROM N.A.
RC MEDLINE=99415938; PubMed=10485905;
RA Holmskov U., Mollerhauer J., Madsen J., Vitved L., Gronlund J.,
RA Tornoe I., Kliehm A., Reid K.B., Poulsen A., Skjoldt K.;
RT "Cloning of gp-340, a putative opsonin receptor for lung surfactant
RT protein D";
RL Proc. Natl. Acad. Sci. U.S.A. 96:10794-10799(1999).
CC -!- SIMILARITY: CONTAINS 2 CUB DOMAINS.
DR EMBJ; AF159456; AAD49696.1; -.
DR InterPro; IPR000859; CUB domain.
DR InterPro; IPR001507; Endoglin/CD105.
DR InterPro; IPR006141; Intein.
DR InterPro; IPR001190; Srcr_receptor.
DR Pfam; PF00431; CUB; 2.
DR Pfam; PF00530; SRCR; 14.
DR Pfam; PF00100; zona_pellucida; 1.
DR PRINTS; PR00258; SPERACTRCPTR.
DR SMART; SM00042; CUB; 2.
DR SMART; SM00202; SR; 14.
DR SMART; SM0241; ZP; 1.
DR TIGRfams; TIGR01443; Intein_Cterm; 12.
DR PROSITE; PS01180; CUB; 2.
DR PROSITE; PS00420; SRCR_1; 13.

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DR PROSITE; PS0287; SRCR_2; 24.
 DR PROSITE; PS0682; ZP_DOMAIN; 1.
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 Query Match 52.3%; Score 46; DB 4; Length 2413;
 Best Local Similarity 64.3%; Pred. No. 1.3e+02;
 Matches 9; Conservative 2; Mismatches 1; Indels 2; Gaps 1;
 QY 4 PSQNGC--LYSSG 15
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 DB 1762 PSSNCGFLFYASG 1775
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 AC Q9UGM3;
 DT 01-MAY-2000 (TrEMBLrel. 13, Created);
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update);
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update);
 DE DMBT1 prototype precursor.
 GN DMBT1.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA MEDLINE=20065089; PubMed=10597221;
 RX Mollenhauer J., Holmskov U., Wiemann S., Krebs I., Herbertz S.,
 RA Madsen J., Kischis P., Coy J.F., Pousterka A.;
 RT "The genomic structure of the DMBT1 gene: evidence for a region with
 RT susceptibility to genomic instability";
 RL Oncogene 18:6233-6240(1999).
 CC -|- SIMILARITY: CONTAINS 2 CUB DOMAINS.
 DR EMBL; AJ243211; CAB63941.1; --
 DR Genew; HGNC:2926; DMBT1.
 DR InterPro; IPR000859; CUB domain.
 DR InterPro; IPR001507; Endoglin/CD105.
 DR InterPro; IPR006141; Intein.
 DR InterPro; IPR001190; Srcr_receptor.
 DR Pfam; PF00431; CUB; 2.
 DR Pfam; PF00510; SRCR; 14.
 DR Pfam; PF00100; zona_pellucida; 1.
 DR PRINTS; PS00258; SPERACTRCPT.
 DR SMART; SM00042; CUB; 2.
 DR SMART; SM00202; SR; 14.
 DR SMART; SM00241; ZP; 1.
 DR TIGRFAMS; TIGR01443; intein_cterm; 13.
 DR PROSITE; PS01180; CUB; 2.
 DR PROSITE; PS00420; SRCR_1; 13.
 DR PROSITE; PS0287; SRCR_2; 14.
 DR PROSITE; PS00692; ZP_DOMAIN; 1.
 KW Signal.
 FT CHAIN 26 2426 DMBT1 PROTOCTYPE.
 FT SIGNAL 26 2426 DMBT1 PROTOCTYPE.
 SQ SEQUENCE 2426 AA; 262052 MW; 5A58FBC076F7247 CRC64;
 Query Match 52.3%; Score 46; DB 4; Length 2426;
 Best Local Similarity 64.3%; Pred. No. 1.3e+02;
 Matches 9; Conservative 2; Mismatches 1; Indels 2; Gaps 1;
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 DB 1775 PSSNCGFLFYASG 1788
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 RESULT 12
 Q8TAE0 PRELIMINARY; PRT; 183 AA.
 ID Q8TAE0
 AC Q8TAE0;
 DT 01-JUN-2002 (TrEMBLrel. 21, Created)
 DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)

DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update);
 FE Keyt binding protein 2.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA TISSUE=Lymph node;
 RA Li R., Han R., Wang C.;
 RT "KSP, a novel protein interacting with LIM protein Koyt.";
 RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF493784; AM12863.1; --
 DR EMBL; AF493786; AM12866.1; --
 SQ SEQUENCE 183 AA; 20207 MW; 872DDE78B01C513B CRC64;
 Query Match 51.1%; Score 45; DB 4; Length 183;
 Best Local Similarity 66.7%; Pred. No. 13;
 Matches 8; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
 QY 3 YPSGNCGLYSS 14
 |||||
 DB 95 YTSQCGKYSS 106
 |||||
 RESULT 13
 Q8NBS2 PRELIMINARY; PRT; 210 AA.
 ID Q8NBS2
 AC Q8NBS2;
 DT 01-OCT-2002 (TrEMBLrel. 22, Created)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
 DE Hypothetical protein FLJ90827.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Isogai T., Ota T., Nishikawa T., Hayashi K., Otsuki T., Sugiyama T.,
 RA Suzuki Y., Nagai K., Sugarc S., Ishii S., Kawai-Hio Y., Saito K.,
 RA Yamamoto J., Wakamatsu A., Nakamura Y., Kojima S., Nagahari K.,
 RA Masuho Y., Ota T., Okano K., Yoshikawa Y., Aotsuka S., Sasaki N.,
 RA Hattori A., Okumura K., Iwayanagi T., Nishimiya K.;
 RT "NEDC human cDNA sequencing project";
 RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AK075308; SACC1537.1; --
 KW Hypothetical protein.
 SQ SEQUENCE 210 AA; 23094 MW; 0501CB50787367DC CRC64;
 Query Match 51.1%; Score 45; DB 4; Length 210;
 Best Local Similarity 66.7%; Pred. No. 15;
 Matches 8; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
 QY 3 YPSGNCGLYSS 14
 |||||
 DB 95 YTSQCGKYSS 106
 |||||
 RESULT 14
 Q8TAC6 PRELIMINARY; PRT; 210 AA.
 ID Q8TAC6
 AC Q8TAC6;
 DT 01-JUN-2002 (TrEMBLrel. 21, Created)
 DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
 DE Keyt binding protein 1 (Chromosome 11 open reading frame 17);
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.

RC TISSUE=Lymph node;
 RA Li R., Han H., Wang J.;
 RT "RSP, a novel protein interacting with LIM protein Kcvt."
 RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Kidney;
 RA Strausberg R.;
 RL Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF493783; AAM12862.1; -
 DR EMBL; AF493786; AAM12865.1; -
 DR EMBL; BC030996; AAB30996.1; -
 SQ SEQUENCE 210 AA; 23114 MW; F0CAAI1F16C37967 CRC64;

Query Match 51.1%; Score 45; DB 4; Length 210;
 Best Local Similarity 66.7%; Pred.No. 15;
 Matches 8; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OY 3 YPSGNCGLYSS 14
 |
 Db 95 YTSQCGKYSS 106

RESULT 15

Q8R0Z6 PRELIMINARY; PRT; 457 AA.
 AC Q8R0Z6;
 DT 01-JUN-2002 (TrEMBLrel. 21, Created);
 DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update);
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update);
 DE Similar to angiotensin-related protein 5 (ARP3).
 GN 630404ELLRIK CP ARP3.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
 CX NCBI_TaxID:10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Liver;
 RA Strausberg R.;
 RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Matsumoto S., Saito Y., Yasunaga K., Oike Y., Suda T.;
 RL Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RA Oike Y., Suda T.;
 RT "Molecular cloning of ARP3."
 RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC025904; AAB25904.1; -
 DR EMBL; AB054065; BAB91249.1; -
 DR MGD; MGI:1917976; 630404Ellrik.
 DR InterPro; IPR002181; Fibrinogen_C.
 DR Pfam; PF00147; fibrinogen_C; 1.
 DR PROSITE; PS00514; FIBRINAG_C DOMAIN; 1.
 SQ SEQUENCE 457 AA; 51095 MW; B7C4289E3FEC6C3E CRC64;

Query Match 50.6%; Score 44.5; DB 11; Length 457;
 Best Local Similarity 60.0%; Pred.No. 40;
 Matches 9; Conservative 1; Mismatches 4; Indels 1; Gaps 1;

OY 1 DRYPSGNCGLYSSG 15
 | | | | |
 Db 391 DSY-SGNCLYHRGG 404

Search completed: November 5, 2003, 16:48:00
 Job time : 27.9824 secs

GenCora version 5.1.6
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OX protein - protein search, using sw model

Run on: November 5, 2003, 15:56:26 ; Search time 2.94053 Seconds
(without alignments)
609.684 Million cell updates/sec

Title: US-09-902-563-18
Perfect score: 88
Sequence: 1 DRYPSGNGGLYSSG 15

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1107863 seqs, 158726573 residues

Total number of hits satisfying chosen parameters: 1107863

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARY

Result No.	Score	Query Match	Length	ID	Description
1	89	100.0	15	20	AAW88237 Human prothrombina
2	89	100.0	432	20	AAW88236 Mouse prothrombina
3	88	100.0	439	20	AAW88235 Human prothrombina
4	50	56.8	53	23	ABP34223 Human angiotensin
5	47	53.4	91	22	AAE20347 Human gene 1 encod
6	46	52.3	102	22	ABG25291 Novel human diagn
7	46	52.3	666	19	AAW64590 Human SRCR protein
8	46	52.3	1785	19	AAW64591 Human SRCR protein
9	46	52.3	3460	23	ABB05007 Human reelin prote

10	46	52.3	3461	23	ABB05008 Mouse reelin prote
11	46	52.3	3461	23	ABB57065 Mouse ischaemic co
12	45	52.3	3470	22	ABG25297 Novel human diagn
13	45	51.1	123	22	AAU80079 Apoptin-associatin
14	45	51.1	126	22	AAU80078 Apoptin-associatin
15	45	51.1	126	23	AAO14806 Human apoptin-asso
16	45	51.1	158	21	ABM42752 Human ORF2516
17	45	51.1	210	22	AAJ30085 Apoptin-associatin
18	45	51.1	210	22	AAW93904 Human polyepitide,
19	45	51.1	210	23	ABP43815 CEGP1 protein #1.
20	45	51.1	210	24	AAE33640 Human BCL3 protein
21	44	50.0	292	22	ABB70950 Drosophila melanog
22	43	48.9	293	24	AAE32106 Human cytoskeleton
23	43	48.9	460	20	AAJ34589 Chlamydia pneumonia
24	42.5	48.3	193	18	AAW55378 H. pylori ORF 07cp
25	42.5	48.3	193	23	AAW50313 Helicobacter pylor
26	42.5	48.3	493	18	AAW55517 H. pylori CRF 07ce
27	42.5	48.3	493	23	AAW50311 Helicobacter pylor
28	42.5	48.3	696	18	AAW55698 H. pylori CRF 14gp
29	42.5	48.3	696	20	AAJ17207 H. pylori outer me
30	42.5	48.3	696	23	AAW50309 Helicobacter pylor
31	42.5	48.3	696	23	AAW50310 Helicobacter pylor
32	41.5	47.2	219	24	AAE32350 Human NL8 fibrinog
33	41.5	47.2	229	22	AAV72625 Human angiotensin
34	41.5	47.2	342	22	AAV72626 Human angiotensin
35	41.5	47.2	470	20	AAV05398 Human TIE ligand N
36	41.5	47.2	470	21	AAW24389 Human PRO178 prote
37	41.5	47.2	470	22	AAW51330 Human angiotensin
38	41.5	47.2	470	22	AAW53066 Human angiotensin
39	41.5	47.2	470	23	ABG80357 Human TIE ligand N
40	41.5	47.2	470	23	ABW95424 Human angiotensin
41	41.5	47.2	470	23	AAE19827 Human TIE ligand N
42	41.5	47.2	470	23	ABW84818 Human PRO178 prote
43	41	46.6	59	17	AAWCS340 Callisoga spider ve
44	41	46.6	39	17	AAWCS341 Callisoga spider ve
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ALIGNMENTS

RESULT 1
AAW88237
ID AAW88237 standard; Peptide; 15 AA.

AC AAW88237;

DT 15-MAR-1999 (first entry;

DE Human prothrombinase Fg12 epitope.

KW Prothrombinase; hfg12; Fg12; human; immune coagulation; antibody;
KW inhibitor; infection; graft rejection; glomerulonephritis; cancer;
KW gastrointestinal disease; foetal loss; therapy; vaccine; epitope.

OS Homo sapiens.

PK WC985.335-AA.

PD 19-NOV-1998.

PF 15-MAY-1998; 98MO-CA00475.

PR 10-CCT-1997; 97JS-0061684.

PR 15-MAY-1997; 97US-0046537.

(LEVY); LEVY G.

Levy G;

XX WPI; 1999-059687/05.

XX Modulating immune coagulation - by using Fg-2 antibodies and

PT compounds, used to treat conditions including graft rejection and
PT foetal loss
XX
XX PS Claim 4; Page 72; 105pp; English.
XX
XX CC This peptide corresponds to amino acid residues 364-378 of human
XX prothrombinase Fg12 (see AAW8235). A claimed method of preventing
XX or treating a condition requiring a reduction in immune
XX coagulation comprises administering an inhibitor of Fg12. The
XX inhibitor is preferably an antibody that binds to the Fg12 epitope.
XX The condition to be treated in graft rejection of foetal loss
XX (claimed).
XX
XX SQ Sequence 15 AA;
Query Match 100.0%; Score 88; DB 20; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.2e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 DRYPSGNCGLYSSG 15
DB 1 DRYPSGNCGLYSSG 15
RESULT 2
AAW8236
ID AAW8236 standard; Protein; 432 AA.
XX
XX AC AAW8236;
XX
XX DT 15-MAR-1999 (first entry);
XX
XX DE Mouse prothrombinase Fg12 protein.
XX
XX KW Prothrombinase; Fg12; mouse; immune coagulation; antibody;
XX inhibitor; infection; graft rejection; glomerulonephritis; cancer;
XX gastrointestinal disease; foetal loss; therapy; vaccine.
XX
XX OS Mus sp.
XX
XX FH Key Location/Qualifiers
XX FT Modified-site 172..174
XX FT /label= Asn is N-glycosylated
XX FT 228..231
XX FT /note= "Asn is N-glycosylated"
XX FT 256..259
XX FT /note= "Asn is N-glycosylated"
XX FT 323..325
XX FT /note= "Asn is N-glycosylated"
XX FT 213..439
XX FT /note= "fibrinogen related domain"
XX
XX PN WO9851335-A1.
XX
XX PD 19-NOV-1998.
XX
XX PF 15-MAY-1998; 98WO-CA00475.
XX
XX PR 10-OCT-1997; 97US-0061684.
XX PR 15-MAY-1997; 97US-0046537.
XX
XX PA (LEVY/) LEVY G.
XX
XX P- Levy G;
XX
XX DR WPI: 1999-059687/05.
XX DR N-PSDB; AAW84140.
XX
XX PT Modulating immune coagulation - by using Fg12 antibodies and
XX compounds, used to treat conditions including graft rejection and
XX foetal loss
XX
XX PS Claim 8; Page 70-71; 105pp; English.

XX
XX CC This is the amino acid sequence of mouse prothrombinase Fg12, as
XX predicted from Fg12 DNA (see AAW84140). Fg12 is a 70 kDa
XX transmembrane serine protease that has immune procoagulant activity.
XX The human Fg12 amino acid sequence is given in AAW8236. The
XX invention provides a method for inhibiting immune coagulation by
XX inhibiting the activity or expression of Fg12. The method can be
XX used in vivo to treat a condition which requires a reduction in
XX immune coagulation such as bacterial and viral infections, cancer,
XX glomerulonephritis, a number of gastrointestinal diseases,
XX allograft and xenograft rejection and foetal loss. An Fg12-specific
XX antibody, an Fg12 antisense oligonucleotide, or a substance that
XX affects prothrombinase activity of a Fg12 protein may be used to
XX treat a condition requiring a reduction in procoagulant activity.
XX A vaccine containing an Fg12 protein or peptide is used for
XX prevention of graft rejection or foetal loss (claimed).
XX
XX SQ Sequence 432 AA;
Query Match 100.0%; Score 88; DB 20; Length 432;
Best Local Similarity 100.0%; Pred. No. 3.5e-05;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 DRYPSGNCGLYSSG 15
DB 357 DRYPSGNCGLYSSG 371
RESULT 3
AAW8235
ID AAW8235 standard; Protein; 439 AA.
XX
XX AC AAW8235;
XX
XX DT 15-MAR-1999 (first entry)
XX
XX DE Human prothrombinase Fg12 protein.
XX
XX KW Prothrombinase; hfg12; Fg12; human; immune coagulation; antibody;
XX inhibitor; infection; graft rejection; glomerulonephritis; cancer;
XX gastrointestinal disease; foetal loss; therapy; vaccine.
XX
XX OS Homo sapiens.
XX
XX FH Key Location/Qualifiers
XX FT Modified-site 179..183
XX FT /label= Asn is N-glycosylated
XX FT 235..238
XX FT /note= "Asn is N-glycosylated"
XX FT 262..265
XX FT /note= "Asn is N-glycosylated"
XX FT 336..337
XX FT /note= "Asn is N-glycosylated"
XX FT 213..439
XX FT /note= "fibrinogen related domain"
XX FT 364..378
XX FT /note= "epitope (Claim 4)"
XX
XX PN WC9851335-A1.
XX
XX PD 19-NOV-1998.
XX
XX PF 15-MAY-1998; 98WO-CA00475.
XX
XX PR 10-OCT-1997; 97US-0061684.
XX PR 15-MAY-1997; 97US-0046537.
XX
XX PA (LEVY/) LEVY G.
XX
XX P- Levy G;
XX
XX DR WPI: 1999-059687/05.
XX DR N-PSDB; AAW84139.

XX Modulating immune coagulation - by using Fgl2 antibodies and
 PT compounds, used to treat conditions including graft rejection and
 PT foetal loss
 XX
 PS Claim 5: Page 66-67; 105pp; English.
 XX
 CC This is the amino acid sequence of human prothrombinase Fgl2, as
 CC predicted from hfgl2 DNA (see AAV841139). Fgl2 is a 7C kDa
 CC transmembrane serine protease that has immune procoagulant activity.
 CC The invention provides a method for inhibiting immune coagulation by
 CC inhibiting the activity or expression of Fgl2. The method can be
 CC used in vivo to treat a condition which requires a reduction in
 CC immune coagulation such as bacterial and viral infections, cancer,
 CC glomerulonephritis, a number of gastrointestinal diseases,
 CC allograft and xenograft rejection and foetal loss. An Fgl2-specific
 CC antibody, an Fgl2 antisense oligonucleotide, or a substance that
 CC affects prothrombinase activity of a Fgl2 protein may be used to
 CC treat a condition requiring a reduction in procoagulant activity.
 CC A vaccine containing an Fgl2 protein or peptide is used for
 CC prevention of graft rejection or foetal loss (claimed).
 XX
 SQ Sequence 439 AA;
 Query Match 100.0%; Score 88; DB 20; Length 439;
 Best Local Similarity 100.0%; Pred. No. 3.6e-05;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Oy 1 DRYPSGNCGLYSSG 15
 |||||
 Db 364 DRYPSGNCGLYSSG 378
 |||||
 RESULT 4
 ABP34223
 ID ABP34223 standard; Protein: 53 AA.
 XX
 AC ABP34223;
 XX
 DT 09-JUL-2002 (first entry)
 XX
 DE Human angiopoietin-like ORF3196 protein, SEQ ID NO:6302.
 XX
 KW Human; ORF: open reading frame; ORFX: drug screening; diagnosis;
 KW disease monitoring; cytokine: cell proliferation; cell differentiation;
 KW immune modulation; haematopoiesis regulation; tissue growth;
 KW angiogenesis; activin; inhibin; chemotactic; chemokinetic; haemostatic;
 KW thrombolytic; tumour inhibition; bodily characteristic; fertility;
 KW behaviour; cancer; proliferative disorder; neurological disorder;
 KW cardiovascular disease; immune system disorder; organ transplantation;
 KW tissue growth disorder; tissue regeneration disorder; diabetes mellitus;
 KW hypothyroidism; cholesterol ester storage disease; infection; vulvovaginitis;
 KW vasotropic; antipsoriatic; antidiabetic; cytostatic; neurotropic;
 KW neuroprotective; antithrombotic; anticoagulant; thrombolytic;
 KW cardiant; hypotensive; antithyroid; antiinflammatory; immunomodulator;
 KW dermatological; analgesic; virucide; antibacterial; fungicide.
 XX
 OS Homo sapiens.
 XX
 PN WO200190366-A2.
 XX
 PD 29-NOV-2001.
 XX
 PF 24-MAY-2001; 2001WO-US17076.
 XX
 PR 24-MAY-2000; 2000US-206690P.
 XX
 PA (CURA-) CURAGEN CORP.
 XX
 PI Leach MD, Shinkets RA;
 XX
 XX WPI; 2002-106200/14.
 DR N-PSDB; ABN78249.

XX Novel human polypeptides and polynucleotides useful for diagnosing,
 PT preventing and treating cardiovascular disease, neurodegenerative,
 PT hyperproliferative disorders and disorders related to organ
 PT transplantation
 XX
 PS Claim 10: Page 1846; 2508pp; English.
 XX
 CC Sequences ABP31028-ABP35561 represent 4534 novel human proteins
 CC designated ORF (Open reading frame) 1-4534, and sequences ABK75054-
 CC ABN75887 represent cDNAs encoding them. The invention also encompasses
 CC polypeptides at least 80% identical to the ORF1-ORF4534 (collectively
 CC referred to as ORFX) proteins, polynucleotides at least 85% identical to
 CC the ORFX nucleic acid sequences, vectors and host cells comprising ORFX
 CC polynucleotides, the recombinant production of ORFX proteins, antibodies
 CC specific for ORFX proteins, methods of detecting ORFX polynucleotides and
 CC polypeptides, methods of screening for modulators of ORFX expression or
 CC activity, and methods of screening individuals for a predisposition to an
 CC ORFX-associated disorder. The ORFX proteins of the invention have a wide
 CC range of biological activities, such as cytokine, cell proliferation,
 CC cell differentiation, immune modulation, haematopoiesis regulation,
 CC tissue growth, angiogenesis, activin or inhibin activity, chemotactic/
 CC chemokinetic activity, haemostatic activity, thrombolytic activity,
 CC receptor/ligand, antiinflammatory activity, tumour inhibition activity,
 CC and antiinfective activity, and may also be involved in the determination
 CC of bodily characteristics, fertility and behaviour. ORFX proteins,
 CC other proliferative disorders such as psoriasis and benign tumours,
 CC neurologic disorders such as epilepsy and Alzheimer's disease,
 CC cardiovascular diseases, immune system disorders, disorders related to
 CC organ transplantation, disorders of tissue growth and regeneration,
 CC diseases such as diabetes mellitus, hypothyroidism, and cholesterol ester
 CC storage disease, and infectious diseases caused by viral, bacterial,
 CC fungal and other pathogens. ORFX nucleic acids may also be used as a
 CC source of primers and probes, in the detection of ORFX genomic sequences
 CC or transcripts, in the identification and cloning of homologous
 CC sequences, in genetic diagnosis, and in forensic biology. The ORFX
 CC nucleic acids may additionally be used to produce transgenic animals
 CC which may be useful for studying the function and/or activity of ORFX
 CC protein, and in drug screening. The ORFX proteins may also be used as
 CC immunogens to generate specific antibodies, which are useful in the
 CC diagnosis, treatment and monitoring of ORFX-associated diseases.
 XX
 SQ Sequence 53 AA;
 Query Match 56.8%; Score 50; DB 23; Length 53;
 Best Local Similarity 56.7%; Pred. No. 2.4;
 Matches 8; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
 Oy 4 PSNGCGLYYSSG 15
 |||||
 Db 20 PSNGCALYHRGG 31
 |||||
 RESULT 5
 AAEO3147
 ID AAEO3147 standard; peptide; 93 AA.
 XX
 AC AAEO3147;
 XX
 DT 10-AUG-2001 (first entry)
 XX
 DE Human gene 1 encoded secreted protein fragment, SEQ ID NO:122.
 XX
 KW Human; secreted protein; proliferative disorder; cancer; tumour;
 KW foetal abnormality; developmental abnormality; haematopoietic disorder;
 KW immune system disorder; AIDS; autoimmune disease; rheumatoid arthritis;
 KW inflammation; allergy; neurological disorder; Alzheimer's disease;
 KW Parkinson's disease; cognitive disorder; schizophrenia; asthma;
 KW skin disorder; psoriasis; sepsis; diabetes; atherosclerosis;
 KW cardiovascular disorder; angioecic disorder; kidney disorder;
 KW gastrointestinal disorder; pregnancy-related disorder;
 KW endocrine disorder; infection; wound healing; vulvovaginitis.

KW cell culture; chemotaxis; food additive; gene therapy;
 KW binding partner identification.

CS Homo sapiens.

XX Key Location/Qualifiers

FT Misc-difference 7 /label= Unknown
 FT FT /note= "X equals stop translation"

PN W02001349C0-A1.

XX 17-MAY-2001.

XX 09-NOV-2000; 2000WO-US30674.

XX 12-NOV-1999; 99US-0164750.

PR 30-JUN-2000; 2000US-0215128.

XX (HUMA-) HUMAN GENOME SCI INC.

PA Ruben SM, Komatsoulis GA, Ebner R, Fiscella M, Wei F;

PI WPI; 2001-329385/34.

XX New nucleic acid molecules encoding human secreted proteins, used in
 PT preventing, treating or ameliorating a disorder, e.g. Alzheimer's and
 PT Parkinson's diseases and cancers -

XX Disclosure; Page 501; 530pp; English.

XX AAD07705-AAD07759 represent cDNAs corresponding to 13 human secreted
 CC protein genes, and AAB03342-AAB03346 represent the proteins they encode.
 CC AAE03347-AAB03375 represent human secreted protein fragments or variants.
 CC The genes and their secreted proteins are useful for preventing,
 CC treating or ameliorating medical conditions, e.g., by protein or gene
 CC therapy. Pathological conditions can be diagnosed by determining the
 CC amount of the new protein in a sample or by determining the presence of
 CC mutations in the new genes. Specific uses are described for each of the
 CC 19 genes, based on the tissues in which they are most highly expressed,
 CC and include developing products for the diagnosis or treatment of
 CC proliferative disorders, cancer, tumours, foetal and developmental
 CC abnormalities, haematopoietic disorders, diseases of the immune system,
 CC AIDS, autoimmune diseases (e.g., rheumatoid arthritis), inflammation,
 CC allergies, neurological disorders (e.g., Alzheimer's disease,
 CC Parkinson's disease), cognitive disorders, schizophrenia, asthma,
 CC skin disorders (e.g., psoriasis), sepsis, diabetes, atherosclerosis,
 CC cardiovascular disorders, angiogenic disorders, kidney disorders,
 CC gastrointestinal disorders, pregnancy-related disorders, endocrine
 CC disorders, and infections. The proteins can also be used to aid wound
 CC healing and epithelial cell proliferation, to prevent skin aging due to
 CC sunburn, to maintain organs before transplantation, for supporting cell
 CC culture of primary tissues, to regenerate tissues, to identify their
 CC cognate ligands or binding partners, and in chemotaxis, and can be used
 CC as a food additive or preservative to modify storage properties.
 CC Antibodies specific for a protein of the invention can be used in
 CC alleviating symptoms associated with the disorders mentioned above, and
 CC in diagnostic immunoassays e.g., radioimmunoassay or enzyme linked
 CC immunosorbent assay (ELISA). The present sequence represents a human
 CC secreted protein fragment referred to in the disclosure of the invention.

XX Sequence 93 AA;

Query Match 53.4%; Score 47; DB 22; Length 93;
 Best Local Similarity 66.7%; Pred. No. 12;
 Matches 8; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

CY 4 PSNCGLYVSSG 15

DB 32 PSNCALYQRGG 43

RESULT 6

ABG25291
 ID ABG25291 standard; Protein; 102 AA.

XX AC ABG25291;

XX DT 18-FEB-2002 (first entry)

XX DE Novel human diagnostic protein #25282.

XX KW Human; chromosome mapping; gene mapping; gene therapy; forensic;
 KW food supplement; medical imaging; diagnostic; genetic disorder.

XX CS Homo sapiens.

XX FN WC200175067-A2.

XX PD 11-OCT-2001.

XX PF 30-MAR-2001; 2001WO-US08631.

XX PR 31-MAR-2000; 2000US-0540217.

XX PR 23-AUG-2000; 2000US-0649167.

XX PA (HYSE-) HYSEQ INC.

XX PI Drmanac XT, Liu C, Tang YT;

XX DR WPI; 2001-639362/73.

XX DR N-ESDB; AAS89478.

XX New isolated polynucleotide and encoded polypeptides, useful in
 PT diagnostics, forensics, gene mapping, identification of mutations
 PT responsible for genetic disorders or other traits and to assess
 PT biodiversity -

XX Claim 20; SEQ ID No 55650; 103pp; English.

XX The invention relates to isolated polynucleotide (I) and
 CC polypeptide (II) sequences. (I) is useful as hybridisation probes,
 CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome
 CC and gene mapping, and in recombinant production of (II). The
 CC polynucleotides are also used in diagnostics as expressed sequence tags
 CC for identifying expressed genes. (I) is useful in gene therapy techniques
 CC to restore normal activity of (II) or to treat disease states involving
 CC (II). (II) is useful for generating antibodies against it, detecting or
 CC quantitating a polypeptide in tissue, as molecular weight markers and as
 CC a food supplement. (I) and its binding partners are useful in medical
 CC imaging of sites expressing (II). (I) and (II) are useful for treating
 CC disorders involving aberrant protein expression or biological activity.
 CC The polypeptide and polynucleotide sequences have applications in
 CC diagnostics, forensics, gene mapping, identification of mutations in
 CC responsible for genetic disorders or other traits to assess biodiversity
 CC and to produce other types of data and products dependent on DNA and
 CC amino acid sequences. ABG0010-ABG0377 represent novel human
 CC diagnostic amino acid sequences of the invention.

CC Note: The sequence data for this patent did not appear in the printed
 CC specification, but was obtained in electronic format directly from WIPC
 CC at ftp.wipo.int/pub/published_pat_sequences.

XX Sequence 102 AA;

Query Match 52.3%; Score 46; DB 22; Length 102;
 Best Local Similarity 71.4%; Pred. No. 18;
 Matches 10; Conservative 0; Mismatches 2; Indels 2; Gaps 1;

CY 3 YPSNCGLY--YSS 14

DB 86 YPSNIGLYCPYSS 99

RESULT 7

AAW64590

ID AAW64590 standard; Protein; 666 AA.


```

DR WPI; 2002-096596/13.
DR N-PSDB; ABA92604.
XX
PT Novel composition useful for screening compounds that modulate Reelin
PT binding to low density lipoprotein receptor, comprising an isolated
PT Reelin polypeptide and low density lipoprotein receptor -
XX
XX Claim 16; Column 31-48; 45pp; English.
XX
CC The present invention describes a composition (I) comprising an
CC isolated reelin protein (II) bound to an isolated low density lipoprotein
CC receptor (LDLR) (III). (II) is an extracellular glycoprotein of
CC approximately 385 kDa containing a small region of similarity with
CC F-spondin at the N terminus, a stretch of positively charged amino
CC acids at the C terminus, and a series of eight internal repeats of
CC 350-390 amino acids, each repeat containing two related sub-domains
CC that flank a pattern of conserved cysteine residues known as an
CC epidermal growth factor (EGF)-like motif. (I) has neuroprotective,
CC neurotropic and antilipemic activities, and can be used as a modulator
CC of reelin-LDLR interaction. (I) is useful in screen for compounds that
CC modulate reelin binding to an LDLR, in an assay system, where the assay
CC system comprises a microplate array and an automated robotic
CC microprocessor controlled system for adding and removing reagents to
CC the microplate array. The compounds identified by the above screening
CC method are useful as therapeutic agents to provide or alleviate a
CC diverse spectrum of diseases including neurodegenerative disorders such
CC as Alzheimer's disease, to facilitate neuronal regeneration after
CC injury, to prevent or alleviate lipid metabolism diseases, to enhance
CC cognitive functions and memory or to ameliorate other developmental
CC disorders. The present sequence represents human reelin, which is used
CC in the exemplification of the present invention.
XX
SQ Sequence 3460 AA;
Query Match 52.3%; Score 46; DB 23; Length 3460;
Best Local Similarity 71.4%; Pred. No. 6.3e+02;
Matches 10; Conservative 0; Mismatches 2; Indels 1;
Gaps 1;
QY 3 YPSGNGCLY--YSS 14
||| ||| |||
Db 1973 YPGGNIGLYCPYSS 1986
||| ||| |||
RESULT 10
AB050038
ID AB050008 standard; Protein; 3461 AA.
XX
AC AB050008;
XX
DT 21-MAR-2002 (first entry)
XX
DE Mouse reelin protein SEQ ID NO:2.
XX
KW Mouse; reelin; low density lipoprotein receptor; LDLR; neuroprotective;
KW extracellular glycoprotein; neurotropic; antilipemic; Alzheimer's disease;
KW neurodegenerative disorder; neuronal regeneration; cognitive function;
KW lipid metabolism disease; memory; developmental disorder.
XX
OS Mus musculus.
XX
PN US6323177-B1.
XX
PD 27-NOV-2001.
XX
PF 16-JUN-1999; 99US-0334220.
XX
PG 16-JUN-1999; 99US-0334220.
XX
PA (SJUD-) ST JUDE CHILDREN'S RES HOSPITAL.
XX
PI Curtán T, D'Arcangelo G;
XX
WPI; 2002-096596/13.

```

```

DR N-PSDB; ABA92603.
XX
PT Novel composition useful for screening compounds that modulate Reelin
PT binding to low density lipoprotein receptor, comprising an isolated
PT Reelin polypeptide and low density lipoprotein receptor -
XX
XX Claim 16; Column 47-64; 45pp; English.
XX
CC The present invention describes a composition (I) comprising an
CC isolated reelin protein (II) bound to an isolated low density lipoprotein
CC receptor (LDLR) (III). (II) is an extracellular glycoprotein of
CC approximately 385 kDa containing a small region of similarity with
CC F-spondin at the N terminus, a stretch of positively charged amino
CC acids at the C terminus, and a series of eight internal repeats of
CC 350-390 amino acids, each repeat containing two related sub-domains
CC that flank a pattern of conserved cysteine residues known as an
CC epidermal growth factor (EGF)-like motif. (I) has neuroprotective,
CC neurotropic and antilipemic activities, and can be used as a modulator
CC of reelin-LDLR interaction. (I) is useful in screen for compounds that
CC modulate reelin binding to an LDLR, in an assay system, where the assay
CC system comprises a microplate array and an automated robotic
CC microprocessor controlled system for adding and removing reagents to
CC the microplate array. The compounds identified by the above screening
CC method are useful as therapeutic agents to provide or alleviate a
CC diverse spectrum of diseases including neurodegenerative disorders such
CC as Alzheimer's disease, to facilitate neuronal regeneration after
CC injury, to prevent or alleviate lipid metabolism diseases, to enhance
CC cognitive functions and memory or to ameliorate other developmental
CC disorders. The present sequence represents mouse (Mus musculus) reelin,
CC which is used in the exemplification of the present invention.
XX
SQ Sequence 3461 AA;
Query Match 52.3%; Score 46; DB 23; Length 3461;
Best Local Similarity 71.4%; Pred. No. 6.3e+02;
Matches 12; Conservative 0; Mismatches 2; Indels 2; Gaps 1;
QY 3 YPSGNGCLY--YSS 14
||| ||| |||
Db 1974 YPGGNIGLYCPYSS 1987
||| ||| |||
RESULT 11
AB057065
ID AB057065 standard; Protein; 3461 AA.
XX
AC AB057065;
XX
DT 07-MAR-2002 (first entry)
XX
DE Mouse ischaemic condition related protein sequence SEQ ID NO:129.
XX
KW Mouse; ischaemia; compressive ischaemia; occlusive ischaemia;
KW vasospastic ischaemia; ischaemic condition; ischaemic disease.
XX
OS Mus musculus.
XX
PN WO200188188-A2.
XX
PD 22-NOV-2001.
XX
PF 16-MAY-2001; 2001WO-JF04192.
XX
PG 18-MAY-2000; 2000JP-0145977.
XX
PA (UYNI-) UNIV NIHOON SCHOOL JURIDICAL PERSON.
XX
PI Ishikawa K, Asai S, Takahashi Y, Nagata T, Ishii Y;
XX
WPI; 2002-034733/04.
XX
N-PSDB; AB199284.
XX
PT Examining the ischemic condition (e.g. occlusive ischemia) by measuring

```

PT expression levels of particular genes defined in the specification or
PT by determining the expression profile of a gene group comprising these
PT genes -
XX
XX
XX Claim 2; Page 385-400; 2690pp; English.
XX
XX The present invention describes a method for examining ischaemic
XX conditions, comprising measuring the expression levels of particular
XX genes (i) in a test sample or determining the expression profile of a
XX gene group in the sample comprising genes selected from (i). The method
XX is useful for examining the ischaemic condition (e.g. compressive
XX ischaemia, occlusive ischaemia or vasospastic ischaemia) by measuring
XX expression levels of particular genes (AB199242 to AB199312, encoding
XX the protein sequences in AB57026 to AB57374); or by determining the
XX expression profile of a gene group comprising these genes. The
XX expression levels or expression profiles produced by these genes are
XX used as an indicator when screening for ischaemic condition-improving
XX drugs or therapeutics for ischaemic diseases. AB199913 and AB199914
XX represent PCR primers for a mouse ischaemic condition related sequence,
XX which are used in the exemplification of the present invention.
XX
SQ Sequence 3461 AA;
Query Match 52.3%; Score 46; DB 23; Length 3461;
Best Local Similarity 71.4%; Pred. No. 6.3e+02;
Matches 10; Conservative 0; Mismatches 2; Indels 2; Gaps 1;
Qy 3 YPSGNGCLY--YSS 14
||| ||| |||
Db 1974 YFGNIGLYCPYSS 1987

RESULT 12
ABG25297
ID ABG25297 standard; Protein; 3470 AA.
XX
XX ABG25297;
XX
XX 18-FEB-2002 (first entry)
XX
XX Novel human diagnostic protein #25288.
XX
XX Human; chromosome mapping; gene mapping; gene therapy; forensic;
XX food supplement; medical imaging; diagnostic; genetic disorder.
XX
XX Homo sapiens.
XX
XX WO200175067-A2.
XX
XX 11-OCT-2001.
XX
XX 30-MAR-2001; 2001WO-US08631.
XX
XX 31-MAR-2000; 2000JS-C540217.
XX
XX 23-AUG-2000; 2000US-C649167.
XX
XX (HYSE-) HYSEQ INC.
XX
XX Drmanac RT, Liu C, Tang YT;
XX
XX WPI; 2001-639362/73.
XX
XX N-PSDB; AAS89484.
XX
XX New isolated polynucleotide and encoded polypeptides, useful in
XX diagnostics, forensics, gene mapping, identification of mutations
XX responsible for genetic disorders or other traits and to assess
XX biodiversity -
XX
XX Claim 20; SEQ ID No 55656; 103pp; English.
XX
XX The invention relates to isolated polynucleotide (i) and
XX polypeptide (ii) sequences. (i) is useful as hybridisation probes.
XX polymerase chain reaction (PCR) primers, oligomers, and for chromosome

CC and gene mapping, and in recombinant production of (ii). The
CC polynucleotides are also used in diagnostics as expressed sequence tags
CC for identifying expressed genes. (i) is useful in gene therapy techniques
CC to restore normal activity of (ii) or to treat disease states involving
CC (ii). (ii) is useful for generating antibodies against it, detecting or
CC quantitating a polypeptide in tissue, as molecular weight markers and as
CC a food supplement. (ii) and its binding partners are useful in medical
CC imaging of sites expressing (ii). (i) and (ii) are useful for treating
CC disorders involving aberrant protein expression or biological activity.
CC The polypeptide and polynucleotide sequences have applications in
CC diagnostics, forensics, gene mapping, identification of mutations
CC responsible for genetic disorders or other traits to assess biodiversity
CC and to produce other types of data and products dependent on DNA and
CC amino acid sequences. ABG0010-ABG30377 represent novel human
CC diagnostic amino acid sequences of the invention.
CC Note: The sequence data for this patent did not appear in the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pat_sequences.
XX
XX
SQ Sequence 3470 AA;
Query Match 52.3%; Score 46; DB 22; Length 3470;
Best Local Similarity 71.4%; Pred. No. 6.4e+02;
Matches 10; Conservative 0; Mismatches 2; Indels 2; Gaps 1;
Qy 3 YPSGNGCLY--YSS 14
||| ||| |||
Db 1983 YFGNIGLYCPYSS 1996

RESULT 13
AAU80C79
ID AAU80C79 standard; Protein; 123 AA.
XX
XX AAU80C79;
XX
XX 30-JUL-2002 (first entry)
XX
XX Apoptin-associating protein: 5 (AAP-5), partial sequence.
XX
XX Cancer; pACT; cytostatic; immunosuppressive; AAP-5;
XX Apoptin-associating protein 5; p53-independent apoptosis;
XX cell proliferation; cell death; autoimmune disease.
XX
XX Homo sapiens.
XX
XX EP1139768-A2.
XX
XX 04-OCT-2001.
XX
XX 27-MAR-2001; 2001EP-0201137.
XX
XX 27-MAR-2000; 2000EP-0201108.
XX
XX LEAD-; LEADD BV.
XX
XX Noteborn XM, Rohn JL, Damen-van Oorschot AAM;
XX
XX WPI; 2001-657960/76.
XX
XX New apoptin-associating protein 5 for inducing p53-independent
XX apoptosis, or for treating cancer or autoimmune disease -
XX
XX Disclosure; Page 23; 44pp; English.
XX
XX The invention relates to an isolated or recombinant nucleic acid
XX which encodes an apoptin-associating protein 5 (AAP-5) capable of
XX providing apoptosis, or its functional fragment. The nucleic acid, a
XX vector comprising the nucleic acid, or a proteinaceous substance is
XX useful for the induction of p53-independent apoptosis. The pharmaceutical
XX composition comprising the nucleic acid, vector comprising the nucleic
XX acid or the proteinaceous substance is also useful for the induction of
XX p53-independent apoptosis, or for the treatment of a disease where

CC enhanced cell proliferation or decreased cell death is observed, such as
 CC cancer or autoimmune disease. The present sequence represents the
 CC partial amino acid sequence of apoptin-associating protein 5 (AAP-5).
 XX
 SQ Sequence 123 AA;

Query Match 51.1%; Score 45; DB 22; Length 123;
 Best Local Similarity 66.7%; Pred. NO. 31;
 Matches 8; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 3 YPSGNCGLYSS 14
 : | | | | |
 Db 8 YTSSQCGKYSS 19

RESULT 14
 AAU80078
 ID AAU80078 standard; Protein; 126 AA.

XX AAU80078;

DT 30-JUL-2002 (first entry)

DE Apoptin-associating protein 5 (AAP-5).

XX Cancer; pACT; cytostatic; immunosuppressive; AAP-5;
 KW Apoptin-associating protein 5; p53-independent apoptosis;
 KW cell proliferation; cell death; autoimmune disease.

XX Homo sapiens.

PH Key Location/Qualifiers

FT Region 1...3
 FT /notes "Encoded by pACT vector"

FN EP1138768-A2.

PC 04-OCT-2001.

PF 27-MAR-2001; 2001EP-0201137.

PR 27-MAR-2000; 2000EP-0201138.

PA (LEAD-) LEAD BV.

PI Noteborn MHM, Rohn JL, Danen-van Oorschot AAAM;

DR MPI: 2001-657963/76.

DR N-PSDB; ABK50949.

PT New apoptin-associating protein 5 for inducing p53-independent
 PT apoptosis, or for treating cancer or autoimmune disease -

PS Claim 10; Fig 2; 44pp; English.

XX The invention relates to an isolated or recombinant nucleic acid
 CC which encodes an apoptin-associating protein 5 (AAP-5) capable of
 CC providing apoptosis, or its functional fragment. The nucleic acid, a
 CC vector comprising the nucleic acid, or a proteinaceous substance is
 CC useful for the induction of p53-independent apoptosis. The pharmaceuti-
 CC cal composition comprising the nucleic acid, vector comprising the nucleic
 CC acid or the proteinaceous substance is also useful for the induction of
 CC p53-independent apoptosis, or for the treatment of a disease where
 CC enhanced cell proliferation or decreased cell death is observed, such as
 CC cancer or autoimmune disease. The present sequence represents the
 CC amino acid sequence of apoptin-associating protein 5 (AAP-5).
 XX

SQ Sequence 126 AA;

Query Match 51.1%; Score 45; DB 22; Length 126;
 Best Local Similarity 66.7%; Pred. NO. 32;
 Matches 8; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 3 YPSGNCGLYSS 14
 : | | | | |
 Db 11 YTSSQCGKYSS 22

RESULT 15

AAO14806
 ID AAO14806 standard; Protein; 126 AA.

XX AAO14806;

DT 06-JUL-2002 (first entry)

DE Human apoptin-associating protein 5, with pACT expression vector region.

XX Human; pACT expression vector; apoptin-associating protein 5; AAP-5;
 KW AAP-6; p53-independent apoptosis; gene therapy; cancer;
 KW autoimmune disease; apoptosis pathway cascade.

XX Homo sapiens.

OS Synthetic.

PH Key Location/Qualifiers

FT Peptide 1...3
 FT /note= "This region is derived from the multiple cloning
 FT site in the pACT expression vector"

FT Protein 4...126

FT /note= "This region represents the human apoptin-
 FT associating protein 5 (AAP-5)"

FN EP1138765-A1.

PC 04-OCT-2001.

PF 27-MAR-2000; 2000EP-0201108.

PR 27-MAR-2000; 2000EP-0201108.

PA (LEAD-) LEAD BV.

PI Noteborn MHM, Rohn JL, Danen-van Oorschot AAAM;

DR MPI: 2002-012523/02.

DR N-PSDB; AAL42576.

PT New proteins useful for inducing p53-independent apoptosis and for
 PT treating cancer and autoimmune diseases comprises the isolated or
 FT recombinant apoptin-associating proteinaceous substance -

PS Disclosure; Fig 3; 28pp; English.

XX The invention comprises the amino acid and coding sequences of two
 CC apoptin-associating proteins (AAP-5 and AAP-6). The AAP-5/AAP-6 DNA and
 CC protein sequences are useful for inducing p53-independent apoptosis, and
 CC the diagnosis/treatment (gene therapy) of cancer and autoimmune diseases.
 CC The AAP-5/AAP-6 DNA and protein sequences are also useful for finding
 CC additional apoptin-associating proteinaceous substances from the
 CC apoptosis pathway cascade. The present amino acid sequence represents the
 CC human AAP-5 protein (with a region derived from the multiple cloning
 CC site of the pACT expression vector).
 XX

SQ Sequence 126 AA;

Query Match 51.1%; Score 45; DB 23; Length 126;
 Best Local Similarity 66.7%; Pred. NO. 32;
 Matches 8; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 3 YPSGNCGLYSS 14
 : | | | | |
 Db 11 YTSSQCGKYSS 22

Search completed: November 5, 2003, 16:46:00

GenCore version: 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: November 5, 2003, 16:48:06 ; Search time 1.69502 Seconds
(without alignments)
1528.925 Million cell updates/sec

Title: US-09-902-563-13

Perfect score: 88

Sequence: 1 DRYPSGNCGLYSSG 15

Scoring table: BLOSUM62

Gapcp 10.0 , Gapext 0.5

Searched: 644079 seqs, 17174932 residues

Total number of hits satisfying chosen parameters: 644079

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 3%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA.*

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1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep.*
2: /cgn2_6/ptodata/2/pubpaa/PC*_NEW_PUB.pep.*
3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep.*
4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep.*
5: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep.*
6: /cgn2_6/ptodata/2/pubpaa/PCUS_PUBCOMB.pep.*
7: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep.*
8: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep.*
9: /cgn2_6/ptodata/2/pubpaa/US09A_PUBCOMB.pep.*
10: /cgn2_6/ptodata/2/pubpaa/US09B_PUBCOMB.pep.*
11: /cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pep.*
12: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep.*
13: /cgn2_6/ptodata/2/pubpaa/US10A_PUBCOMB.pep.*
14: /cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep.*
15: /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep.*
16: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep.*
17: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep.*
18: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query	Score	Match	Length	DB ID	Description
1	89	100.0	15	15	US-09-902-563-18	Sequence 18, Appl
2	88	100.0	15	15	US-10-C96-255-18	Sequence 18, Appl
3	88	100.0	432	11	US-09-902-563-4	Sequence 4, Appl
4	88	100.0	432	11	US-10-C96-255-4	Sequence 4, Appl
5	88	100.0	439	11	US-09-902-563-2	Sequence 2, Appl
6	88	100.0	439	15	US-10-C96-255-2	Sequence 2, Appl
7	45	51.1	126	9	US-09-819-308-2	Sequence 2, Appl
8	45	51.1	210	9	US-09-819-308-10	Sequence 10, Appl
9	41.5	47.2	219	11	US-09-832-355A-24	Sequence 24, Appl
10	41.5	47.2	470	12	US-10-394-557-6	Sequence 6, Appl
11	41.5	47.2	470	12	US-10-223-081-4	Sequence 4, Appl
12	41.5	47.2	470	12	US-10-223-082-4	Sequence 4, Appl
13	41.5	47.2	470	15	US-10-223-085-4	Sequence 4, Appl
14	41.5	47.2	470	15	US-10-223-084-4	Sequence 4, Appl
15	41.5	47.2	470	15	US-10-223-088-4	Sequence 4, Appl

16	41.5	47.2	470	15	US-10-223-090-4	Sequence 4, Appl
17	41.5	47.2	470	15	US-10-223-087-4	Sequence 4, Appl
18	41.5	47.2	470	15	US-10-223-083-4	Sequence 4, Appl
19	41.5	47.2	470	15	US-10-223-089-4	Sequence 4, Appl
20	40	45.5	316	14	US-10-001-870-132	Sequence 32, Appl
21	40	45.5	776	10	US-09-908-193-33	Sequence 33, Appl
22	39.5	44.9	99	11	US-09-229-173-29	Sequence 29, Appl
23	39.5	44.9	212	11	US-09-994-595-150	Sequence 150, Appl
24	39.5	44.9	278	12	US-10-220-521-11	Sequence 11, Appl
25	39.5	44.9	517	12	US-10-032-585-7874	Sequence 7874, Appl
26	39.5	44.9	1391	11	US-09-994-595-8	Sequence 8, Appl
27	39	44.3	588	10	US-09-908-193-34	Sequence 34, Appl
28	39	44.3	673	10	US-09-908-193-46	Sequence 46, Appl
29	39	44.3	695	5	US-09-164-898-191	Sequence 191, Appl
30	39	44.3	754	10	US-09-908-193-8	Sequence 32, Appl
31	39	44.3	778	10	US-09-908-193-8	Sequence 9, Appl
32	39	44.3	779	10	US-09-908-193-10	Sequence 10, Appl
33	39	44.3	791	10	US-09-908-193-18	Sequence 18, Appl
34	39	44.3	837	11	US-09-946-374-253	Sequence 253, Appl
35	39	44.3	837	12	US-10-015-387A-253	Sequence 253, Appl
36	39	44.3	837	12	US-10-006-130A-253	Sequence 253, Appl
37	39	44.3	837	12	US-10-199-672-454	Sequence 454, Appl
38	39	44.3	837	12	US-10-241-220-57	Sequence 57, Appl
39	39	44.3	837	12	US-10-006-172A-253	Sequence 253, Appl
40	39	44.3	837	12	US-10-187-749-454	Sequence 454, Appl
41	39	44.3	837	12	US-10-194-457-454	Sequence 454, Appl
42	39	44.3	837	12	US-10-184-642-454	Sequence 454, Appl
43	39	44.3	837	12	US-10-196-747-454	Sequence 454, Appl
44	39	44.3	837	12	US-10-015-392A-253	Sequence 253, Appl
45	39	44.3	837	12	US-10-017-253A-253	Sequence 253, Appl

ALIGNMENTS

RESULT :

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US-09-902-563-18
; Sequence 18, Application US/09902563
; Publication No. US20030099654A1
; GENERAL INFORMATION:
; APPLICANT: Levy, Gary
; TITLE OF INVENTION: Methods of Modulating Immune Coagulation
; FILE REFERENCE: 9579-37
; CURRENT APPLICATION NUMBER: US/09/902.563
; PRIORITY FILING DATE: 2002-09-09
; PRIOR APPLICATION NUMBER: US 09/442,143
; PRIORITY FILING DATE: 1999-11-15
; NUMBER OF SEQ ID NOS: 53
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 18
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-902-563-18
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Query Match 100.0% ; Score 88 ; DB 11 ; Length 15;
Best Local Similarity 100.0% ; Pred. No. 4.9e-07;
Matches 15 ; Conservative 0 ; Mismatches 0 ; Indels 0 ; Gaps 0 ;

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QY 1 DRYPSGNCGLYSSG 15
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DB 1 DRYPSGNCGLYSSG 15
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RESULT: 2

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US-10-096-255-18
; Sequence 18, Application US/10036255
; Publication No. US20030103974A1
; GENERAL INFORMATION:
; APPLICANT: Levy, Gary
; APPLICANT: Clark, David A.
; TITLE OF INVENTION: Methods of Modulating Immune Coagulation
; FILE REFERENCE: 9579-52
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; CURRENT APPLICATION NUMBER: US/10/096,255
; CURRENT FILING DATE: 2002-03-13
; PRIOR APPLICATION NUMBER: US 60/046,537
; PRIOR FILING DATE: 1997-05-17
; PRIOR APPLICATION NUMBER: US 60/061,684
; PRIOR FILING DATE: 1997-10-10
; NUMBER OF SEQ ID NOS: 53
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 18
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-096-255-18

Query Match      100.0%; Score 88; DB 15; Length 15;
Best Local Similarity 100.0%; Pred. No. 4.9e-07;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 DRYPSGNCGLYYSSG 15
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Db      357 DRYPSGNCGLYYSSG 371

RESULT 3
US-09-902-563-4
; Sequence 4, Application US/09902563
; Publication No. US20030099654A1
; GENERAL INFORMATION:
; APPLICANT: Levy, Gary
; TITLE OF INVENTION: Methods of Modulating Immune Coagulation
; CURRENT APPLICATION NUMBER: US/09/902,563
; CURRENT FILING DATE: 2002-09-09
; PRIOR APPLICATION NUMBER: US 09/442,143
; PRIOR FILING DATE: 1999-11-15
; NUMBER OF SEQ ID NOS: 53
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 432
; TYPE: PRT
; ORGANISM: Murine fgl2
US-09-902-563-4

Query Match      100.0%; Score 88; DB 11; Length 432;
Best Local Similarity 100.0%; Pred. No. 1.3e-05;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 DRYPSGNCGLYYSSG 15
      |||||
Db      357 DRYPSGNCGLYYSSG 371

RESULT 4
US-10-096-255-4
; Sequence 4, Application US/10096255
; Publication No. US20030103974A1
; GENERAL INFORMATION:
; APPLICANT: Levy, Gary
; TITLE OF INVENTION: Methods of Modulating Immune Coagulation
; FILE REFERENCE: 9579-52
; CURRENT APPLICATION NUMBER: US/10/096,255
; CURRENT FILING DATE: 2002-03-13
; PRIOR APPLICATION NUMBER: US 60/046,537
; PRIOR FILING DATE: 1997-05-17
; PRIOR APPLICATION NUMBER: US 60/061,684
; PRIOR FILING DATE: 1997-10-10
; NUMBER OF SEQ ID NOS: 53
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 432
; TYPE: PRT
; ORGANISM: Murine fgl2
US-10-096-255-4

Query Match      100.0%; Score 88; DB 11; Length 432;
Best Local Similarity 100.0%; Pred. No. 1.3e-05;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 DRYPSGNCGLYYSSG 15
      |||||
Db      357 DRYPSGNCGLYYSSG 371

RESULT 5
US-03-902-563-2
; Sequence 2, Application US/09902563
; Publication No. US20030099654A1
; GENERAL INFORMATION:
; APPLICANT: Levy, Gary
; TITLE OF INVENTION: Methods of Modulating Immune Coagulation
; FILE REFERENCE: 9579-37
; CURRENT APPLICATION NUMBER: US/09/902,563
; CURRENT FILING DATE: 2002-09-09
; PRIOR APPLICATION NUMBER: US 09/442,143
; PRIOR FILING DATE: 1999-11-15
; NUMBER OF SEQ ID NOS: 53
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 439
; TYPE: PRT
; ORGANISM: Homo sapiens fgl2
US-09-902-563-2

Query Match      100.0%; Score 88; DB 11; Length 439;
Best Local Similarity 100.0%; Pred. No. 1.3e-05;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 DRYPSGNCGLYYSSG 15
      |||||
Db      364 DRYPSGNCGLYYSSG 378

RESULT 6
US-10-096-255-2
; Sequence 2, Application US/10096255
; Publication No. US20030103974A1
; GENERAL INFORMATION:
; APPLICANT: Clark, David A.
; TITLE OF INVENTION: Methods of Modulating Immune Coagulation
; FILE REFERENCE: 9579-52
; CURRENT APPLICATION NUMBER: US/10/096,255
; CURRENT FILING DATE: 2002-03-13
; PRIOR APPLICATION NUMBER: US 60/046,537
; PRIOR FILING DATE: 1997-05-17
; PRIOR APPLICATION NUMBER: US 60/061,684
; PRIOR FILING DATE: 1997-10-10
; NUMBER OF SEQ ID NOS: 53
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 439
; TYPE: PRT
; ORGANISM: Homo sapiens fgl2
US-10-096-255-2

Query Match      100.0%; Score 88; DB 15; Length 439;
Best Local Similarity 100.0%; Pred. No. 1.3e-05;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 DRYPSGNCGLYYSSG 15
      |||||
Db      364 DRYPSGNCGLYYSSG 378

RESULT 7
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US-09-819-308-2
; Sequence 2, Application US/09819308
; Patent No. US20020019040A1
; GENERAL INFORMATION:
; APPLICANT: No. US20020019040A1, Mathieu
; APPLICANT: Danen-van Oorschot, Astrid
; APPLICANT: Rohn, Jennifer
; TITLE OF INVENTION: APOPTIN-ASSOCIATING PROTEIN
; FILE REFERENCE: 2906-4820US
; CURRENT APPLICATION NUMBER: US/09/819,308
; CURRENT FILING DATE: 2001-03-27
; NUMBER OF SEQ ID NOS: 46
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2
; LENGTH: 126
; TYPE: PRT
; ORGANISM: vector pMT2SM-AAP-5
US-09-819-308-2

Query Match 51.1%; Score 45; DB 9; Length 126;
Best Local Similarity 66.7%; Pred. No. 16;
Matches 8; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Cy 3 YPSGNCGLYYSS 14
| | | | |
Db 11 YTSQCCKYYSS 22

RESULT 8
US-09-819-308-10
; Sequence 10, Application US/09819308
; Patent No. US20020019040A1
; GENERAL INFORMATION:
; APPLICANT: No. US20020019040A1, Mathieu
; APPLICANT: Danen-van Oorschot, Astrid
; APPLICANT: Rohn, Jennifer
; TITLE OF INVENTION: APOPTIN-ASSOCIATING PROTEIN
; FILE REFERENCE: 2906-4820US
; CURRENT APPLICATION NUMBER: US/09/819,308
; CURRENT FILING DATE: 2001-03-27
; NUMBER OF SEQ ID NOS: 46
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 10
; LENGTH: 210
; TYPE: PRT
; ORGANISM: open reading frame of AAP-5
US-09-819-308-10

Query Match 51.1%; Score 45; DB 9; Length 210;
Best Local Similarity 66.7%; Pred. No. 26;
Matches 8; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Cy 3 YPSGNCGLYYSS 14
| | | | |
Db 95 YTSQCCKYYSS 106

RESULT 9
US-09-832-355A-24
; Sequence 24, Application US/09832355A
; Publication No. US2003002751A1
; GENERAL INFORMATION:
; APPLICANT: Kovesdi, Imre
; APPLICANT: Kessier, Paul
; TITLE OF INVENTION: VEGF FUSION PROTEINS
; FILE REFERENCE: 205654
; CURRENT APPLICATION NUMBER: US/09/832,355A
; CURRENT FILING DATE: 2001-04-10
; NUMBER OF SEQ ID NOS: 126
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 24
; LENGTH: 219
; TYPE: PRT

; ORGANISM: Homo sapiens
US-09-832-355A-24

Query Match 47.2%; Score 41.5; DB 11; Length 219;
Best Local Similarity 60.0%; Pred. No. 93;
Matches 9; Conservative 0; Mismatches 5; Indels 1; Gaps 1;

Cy 1 DRYPSGNCGLYYSSG 15
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Db 153 DSY-SGNCALYQKGG 166

RESULT 10
US-10-394-557-6
; Sequence 6, Application US/10394557
; Publication No. US20030175289A1
; GENERAL INFORMATION:
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; TITLE OF INVENTION: Tie Ligands
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSES: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080

COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Winpatin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/394,557
FILING DATE: 21-Mar-2003
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/933,821
FILING DATE: 19-SEPT-1997
ATTORNEY/AGENT INFORMATION:
NAME: Dreger, Ginger R.
REGISTRATION NUMBER: 33,055
REFERENCE/DOCKET NUMBER: P1130
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/952-3216
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 470 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
SEQUENCE DESCRIPTION: SEQ ID NO: 6:
US-10-394-557-6

Query Match 47.2%; Score 41.5; DB 12; Length 470;
Best Local Similarity 60.0%; Pred. No. 2e-02;
Matches 9; Conservative 0; Mismatches 5; Indels 1; Gaps 1;

Cy 1 DRYPSGNCGLYYSSG 15
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Db 404 DSY-SGNCALYQKGG 417

RESULT 11
US-10-223-081-4
; Sequence 4, Application US/10223081
; Publication No. US20030196866A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.

```

/ APPLICANT: Goddard, Audrey
/ APPLICANT: Godowski, Paul J.
/ APPLICANT: Gurney, Austin L.
/ APPLICANT: Hillan, Kenneth J.
/ APPLICANT: Marsters, Scott A.
/ APPLICANT: Pan, James
/ APPLICANT: Stephan, Jean-Philippe F.
/ APPLICANT: Watanabe, Colin K.
/ APPLICANT: Wood, William I.
/ APPLICANT: Williams, P. Mickey
/ APPLICANT: Ye, Weilan
/ TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DIAGNOSIS AND
/ FILE REFERENCE: P3235P1C7
/ CURRENT APPLICATION NUMBER: US 10/223,081
/ CURRENT FILING DATE: 2002-08-16
/ PRIOR APPLICATION NUMBER: US 10/081,056
/ PRIOR FILING DATE: 2002-02-20
/ PRIOR APPLICATION NUMBER: US 60/213,637
/ PRIOR FILING DATE: 2000-06-23
/ PRIOR APPLICATION NUMBER: US 60/219,556
/ PRIOR FILING DATE: 2000-07-20
/ PRIOR APPLICATION NUMBER: US 60/220,624
/ PRIOR FILING DATE: 2000-07-25
/ PRIOR APPLICATION NUMBER: PCT/US00/20710
/ PRIOR FILING DATE: 2000-07-28
/ PRIOR APPLICATION NUMBER: US 60/222,695
/ PRIOR FILING DATE: 2000-08-02
/ PRIOR APPLICATION NUMBER: US 09/643,657
/ PRIOR FILING DATE: 2000-08-17
/ PRIOR APPLICATION NUMBER: PCT/US00/23522
/ PRIOR FILING DATE: 2000-08-23
/ PRIOR APPLICATION NUMBER: US 60/220,664
/ PRIOR FILING DATE: 2000-07-25
/ PRIOR APPLICATION NUMBER: PCT/US00/23328
/ PRIOR FILING DATE: 2000-08-24
/ Remaining Prior Application data removed - See File Wrapper or PALM.
/ NUMBER OF SEQ ID NOS: 383
/ SEQ ID NO 4
/ LENGTH: 470
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-10-223-081-4

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Query Match 47.2%; Score 41.5; DB 12; Length 470;
Best Local Similarity 60.0%; Pred. No. 2e+02;
Matches 9; Conservative 0; Mismatches 5; Indels 1; Gaps 1;

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QY 1 DRYFSGNCGLYSSG 15
DB 404 DSY-SGNCALYQSG 417

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RESULT 12
US-10-223-082-4
/ Sequence 4, Application US/10223082
/ Publication No. US20030191059A1
/ GENERAL INFORMATION:
/ APPLICANT: Baker, Kevin P.
/ APPLICANT: Ferrara, Napoleone
/ APPLICANT: Gerber, Hanspeter
/ APPLICANT: Gerritsen, Mary E.
/ APPLICANT: Goddard, Audrey
/ APPLICANT: Godowski, Paul J.
/ APPLICANT: Gurney, Austin L.
/ APPLICANT: Hillan, Kenneth J.
/ APPLICANT: Marsters, Scott A.
/ APPLICANT: Pan, James
/ APPLICANT: Stephan, Jean-Philippe F.
/ APPLICANT: Watanabe, Colin K.
/ APPLICANT: Wood, William I.
/ APPLICANT: Williams, P. Mickey
/ APPLICANT: Ye, Weilan

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/ TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DIAGNOSIS AND
/ FILE REFERENCE: P3235P1C3
/ CURRENT APPLICATION NUMBER: US 10/223,082
/ CURRENT FILING DATE: 2002-08-16
/ PRIOR APPLICATION NUMBER: US 10/081,056
/ PRIOR FILING DATE: 2002-02-20
/ PRIOR APPLICATION NUMBER: US 60/213,637
/ PRIOR FILING DATE: 2000-06-23
/ PRIOR APPLICATION NUMBER: US 60/219,556
/ PRIOR FILING DATE: 2000-07-20
/ PRIOR APPLICATION NUMBER: US 60/220,624
/ PRIOR FILING DATE: 2000-07-25
/ PRIOR APPLICATION NUMBER: PCT/US00/20710
/ PRIOR FILING DATE: 2000-07-28
/ PRIOR APPLICATION NUMBER: US 60/222,695
/ PRIOR FILING DATE: 2000-08-02
/ PRIOR APPLICATION NUMBER: US 09/643,657
/ PRIOR FILING DATE: 2000-08-17
/ PRIOR APPLICATION NUMBER: PCT/US00/23522
/ PRIOR FILING DATE: 2000-08-23
/ PRIOR APPLICATION NUMBER: PCT/US00/23328
/ Remaining Prior Application data removed - See File Wrapper or PALM.
/ NUMBER OF SEQ ID NOS: 383
/ SEQ ID NO 4
/ LENGTH: 470
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-10-223-082-4

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Query Match 47.2%; Score 41.5; DB 12; Length 470;
Best Local Similarity 60.0%; Pred. No. 2e+02;
Matches 9; Conservative 0; Mismatches 5; Indels 1; Gaps 1;

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QY 1 DRYFSGNCGLYSSG 15
DB 404 DSY-SGNCALYQSG 417

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RESULT 13
US-10-223-085-4
/ Sequence 4, Application US/10223085
/ Publication No. US20030130497A1
/ GENERAL INFORMATION:
/ APPLICANT: Baker, Kevin P.
/ APPLICANT: Ferrara, Napoleone
/ APPLICANT: Gerber, Hanspeter
/ APPLICANT: Gerritsen, Mary E.
/ APPLICANT: Goddard, Audrey
/ APPLICANT: Godowski, Paul J.
/ APPLICANT: Gurney, Austin L.
/ APPLICANT: Hillan, Kenneth J.
/ APPLICANT: Marsters, Scott A.
/ APPLICANT: Pan, James
/ APPLICANT: Stephan, Jean-Philippe F.
/ APPLICANT: Watanabe, Colin K.
/ APPLICANT: Wood, William I.
/ APPLICANT: Williams, P. Mickey
/ APPLICANT: Ye, Weilan
/ TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DIAGNOSIS AND
/ FILE REFERENCE: P3235P1C10
/ CURRENT APPLICATION NUMBER: US 10/223,085
/ CURRENT FILING DATE: 2002-08-16
/ PRIOR APPLICATION NUMBER: US 10/081,056
/ PRIOR FILING DATE: 2002-02-20
/ PRIOR APPLICATION NUMBER: US 60/213,637
/ PRIOR FILING DATE: 2000-06-23
/ PRIOR APPLICATION NUMBER: US 60/219,556
/ PRIOR FILING DATE: 2000-07-20

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; PRIOR APPLICATION NUMBER: US 60/220,624
; PRIOR FILING DATE: 2000-07-25
; PRIOR APPLICATION NUMBER: US 60/220,664
; PRIOR FILING DATE: 2000-07-25
; PRIOR APPLICATION NUMBER: PCT/US00/20710
; PRIOR FILING DATE: 2000-07-28
; PRIOR APPLICATION NUMBER: US 60/222,695
; PRIOR FILING DATE: 2000-08-02
; PRIOR APPLICATION NUMBER: US 09/643,657
; PRIOR FILING DATE: 2000-08-17
; PRIOR APPLICATION NUMBER: PCT/US00/23522
; PRIOR FILING DATE: 2000-08-23
; PRIOR APPLICATION NUMBER: PCT/US00/23328
; PRIOR FILING DATE: 2000-08-24
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 363
; SEQ ID NO 4
; LENGTH: 470
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-223-084-4

Query Match          47.2%; Score 41.5; DB 15; Length 470;
Best Local Similarity 60.0%; Pred. No. 2e+02;
Matches 9; Conservative 0; Mismatches 5; Indels 1; Gaps 1;

QY 1 DRYPSGNGGLYSSG 15
DQ 404 DSY-SGNCALYQRGG 417

RESULT 14
US-10-223-084-4
; Sequence 4, Application US/10223084
; Publication No. US20030105011A
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Marsters, Scot A.
; APPLICANT: Pan, James
; APPLICANT: Stephan, Jean-Philippe F.
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Ye, Weilan
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DIAGNOSIS AND
; FILE REFERENCE: P3235PIC5
; CURRENT APPLICATION NUMBER: US 10/223,084
; PRIOR FILING DATE: 2002-08-16
; PRIOR APPLICATION NUMBER: US 10/281,056
; PRIOR FILING DATE: 2000-02-20
; PRIOR FILING DATE: 2000-06-23
; PRIOR APPLICATION NUMBER: US 60/219,556
; PRIOR FILING DATE: 2000-07-20
; PRIOR APPLICATION NUMBER: US 60/220,624
; PRIOR FILING DATE: 2000-07-25
; PRIOR APPLICATION NUMBER: US 60/220,664
; PRIOR FILING DATE: 2000-07-28
; PRIOR APPLICATION NUMBER: PCT/US00/20710
; PRIOR FILING DATE: 2000-07-25
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 363
; SEQ ID NO 4
; LENGTH: 470
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-223-084-4
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; PRIOR FILING DATE: 2000-08-23
; PRIOR APPLICATION NUMBER: PCT/US00/23328
; PRIOR FILING DATE: 2000-08-24
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 383
; SEQ ID NO 4
; LENGTH: 470
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-223-084-4

Query Match          47.2%; Score 41.5; DB 15; Length 470;
Best Local Similarity 60.0%; Pred. No. 2e+02;
Matches 9; Conservative 0; Mismatches 5; Indels 1; Gaps 1;

QY 1 DRYPSGNGGLYSSG 15
DQ 404 DSY-SGNCALYQRGG 417

RESULT 15
US-10-223-088-4
; Sequence 4, Application US/10223088
; Publication No. US20030105012A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Marsters, Scot A.
; APPLICANT: Pan, James
; APPLICANT: Stephan, Jean-Philippe F.
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Ye, Weilan
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DIAGNOSIS AND
; FILE REFERENCE: P3235PIC6
; CURRENT APPLICATION NUMBER: US 10/223,088
; PRIOR FILING DATE: 2002-08-16
; PRIOR APPLICATION NUMBER: US 10/081,056
; PRIOR FILING DATE: 2002-02-20
; PRIOR APPLICATION NUMBER: US 60/213,637
; PRIOR FILING DATE: 2000-06-23
; PRIOR APPLICATION NUMBER: US 60/219,556
; PRIOR FILING DATE: 2000-07-20
; PRIOR APPLICATION NUMBER: US 60/220,624
; PRIOR FILING DATE: 2000-07-25
; PRIOR APPLICATION NUMBER: US 60/220,664
; PRIOR FILING DATE: 2000-07-28
; PRIOR APPLICATION NUMBER: PCT/US00/20710
; PRIOR FILING DATE: 2000-07-26
; PRIOR APPLICATION NUMBER: US 60/222,695
; PRIOR FILING DATE: 2000-08-02
; PRIOR APPLICATION NUMBER: US 09/643,657
; PRIOR FILING DATE: 2000-08-17
; PRIOR APPLICATION NUMBER: PCT/US00/23522
; PRIOR FILING DATE: 2000-08-23
; PRIOR APPLICATION NUMBER: PCT/US00/23328
; PRIOR FILING DATE: 2000-08-24
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 383
; SEQ ID NO 4
; LENGTH: 470
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-223-088-4
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Query Match 47.28; Score 41.5; DB 15; Length 475;
Best Local Similarity 60.0%; Pred. No. 2e-02;
Matches 9; Conservative 0; Mismatches 5; Indels 1; Gaps 1;
Cy 1 DRYPSGNCG:YYSSG 15
Cb 404 DSY-SGNCALYQRGG 417

Search completed: November 5, 2003, 16:56:34
Job time : 1.68502 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 5, 2003, 16:44:23 ; Search time 1.05727 Seconds
(without alignments)
600.285 Million call updates/sec

Title: US-09-902-563-18

Perfect score: 88

Sequence: 1 DRYPSGNGGLYYSSG 15

Scoring table: BLOSUM62

Gapop 10.0 ; Gapext 0.5

Searched: 328717 seqs, 42310858 residues

Total number of hits satisfying chosen parameters: 328717

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA.*
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2: /cgn2_6/prodata/1/iaa/5A_COXB.pep.*
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6: /cgn2_6/prodata/1/iaa/6A_COMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	88	100.0	15	4	US-09-442-143A-18
2	88	100.0	432	4	US-09-442-143A-4
3	88	100.0	439	4	US-09-442-143A-2
4	46	52.3	666	4	US-09-341-587-1
5	46	52.3	1785	4	US-09-341-587-3
6	46	52.3	3460	4	US-09-334-220-1
7	46	52.3	3461	4	US-09-334-220-2
8	43	48.9	460	4	US-09-196-452A-7
9	42	47.7	409	4	US-09-328-352-6858
10	41.5	47.2	470	2	US-08-933-821-6
11	41.5	47.2	470	3	US-08-960-507-6
12	41.5	47.2	470	4	US-09-336-828-6
13	41.5	47.2	470	4	US-09-332-928A-6
14	41.5	47.2	470	4	US-09-336-801-6
15	41.5	47.2	470	4	US-09-332-929-6
16	41.5	47.2	470	4	US-09-333-075-6
17	41.5	47.2	470	4	US-09-302-088A-6
18	41.5	47.2	470	4	US-09-333-077-6
19	41	46.6	39	1	US-08-390-882A-1
20	41	46.6	39	1	US-08-390-882A-2
21	40	45.5	1041	4	US-08-494-714-2
22	40	45.5	1041	5	PCT-US96-10782-2
23	39.5	44.9	39	2	US-08-537-460-19
24	39.5	44.9	212	4	US-09-106-568E-150
25	39.5	44.9	1391	4	US-09-106-568E-8
26	39	44.3	38	1	US-08-451-472-9
27	39	44.3	39	1	US-08-390-882A-3

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28 39 44.3 78 4 US-09-732-210-338 Sequence 338, App
29 39 44.3 79 4 US-09-732-210-343 Sequence 343, App
30 39 44.3 79 4 US-09-732-210-347 Sequence 347, App
31 39 44.3 80 4 US-09-732-210-346 Sequence 346, App
32 39 44.3 81 4 US-09-732-210-337 Sequence 337, App
33 39 44.3 524 4 US-09-198-452A-52 Sequence 52, Appli
34 39 44.3 700 4 US-09-408-647A-2 Sequence 2, Appli
35 39 44.3 1077 4 US-09-390-234-12 Sequence 12, Appli
36 39 44.3 2254 2 US-08-286-819A-28 Sequence 28, Appli
37 39 44.3 2254 3 US-08-980-357-28 Sequence 4, Appli
38 36.5 43.8 406 3 US-09-108-020-4 Sequence 42, Appli
39 38.5 43.8 406 3 US-09-158-020-42 Sequence 23974, A
40 38 43.2 256 4 US-09-252-991A-23974 Sequence 23974, A
41 38 43.2 368 4 US-09-252-991A-27921 Sequence 27921, A
42 38 43.2 438 4 US-09-252-991A-21521 Sequence 21521, A
43 38 43.2 1901 4 US-09-738-946-12 Sequence 12, Appli
44 38 43.2 2465 2 US-08-596-291-3 Sequence 3, Appli
45 38 43.2 2465 3 US-09-100-804-3 Sequence 3, Appli

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ALIGNMENTS

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RESULT 1
US-09-442-143A-18
; Sequence 18, Application US/09442143A
; Patent No. 6403089
; GENERAL INFORMATION:
; APPLICANT: Levy, Gary
; TITLE OF INVENTION: Methods of Modulating Immune Coagulation.
; FILE REFERENCE: 9579-14
; CURRENT APPLICATION NUMBER: US/09/442.143A
; PRIOR FILING DATE: 1999-11-15
; PRIOR APPLICATION NUMBER: US 60/046,537
; PRIOR FILING DATE: 1997-05-17
; PRIOR APPLICATION NUMBER: US 60/061,684
; PRIOR FILING DATE: 1997-10-10
; NUMBER OF SEQ ID NOS: 53
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 18
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-442-143A-18
Query Match 100.0%; Score 88; DB 4; Length 15;
Best Local Similarity 100.0%; Pred. No. 41e-07;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DRYPSGNGGLYYSSG 15
DB 1 DRYPSGNGGLYYSSG 15

RESULT 2
US-09-442-143A-4
; Sequence 4, Application US/09442143A
; Patent No. 6403089
; GENERAL INFORMATION:
; APPLICANT: Levy, Gary
; TITLE OF INVENTION: Methods of Modulating Immune Coagulation
; FILE REFERENCE: 9579-14
; CURRENT APPLICATION NUMBER: US/09/442.143A
; PRIOR FILING DATE: 1999-11-15
; PRIOR APPLICATION NUMBER: US 60/046,537
; PRIOR FILING DATE: 1997-05-17
; PRIOR APPLICATION NUMBER: US 60/061,684
; PRIOR FILING DATE: 1997-10-10
; NUMBER OF SEQ ID NOS: 53
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4

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; LENGTH: 432
; TYPE: PRT
; ORGANISM: Murine fgl2
US-09-442-143A-4

Query Match 100.0%; Score 88; DB 4; Length 432;
Best Local Similarity 100.0%; Pred. No. 1.2e-05;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DRYPSGNCGLYSSG 15
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Db 357 DRYPSGNCGLYSSG 371

RESULT 3

US-09-442-143A-2
; Sequence 2, Application US/09442-43A
; Patent No. 6403089

; GENERAL INFORMATION:
; APPLICANT: Levy, Gary

; APPLICANT: Clark, David A.
; TITLE OF INVENTION: Methods of Modulating Immune Coagulation

; FILE REFERENCE: 9579-14
; CURRENT APPLICATION NUMBER: US/09/442-143A

; CURRENT FILING DATE: 1999-11-15
; PRIOR APPLICATION NUMBER: US 60/046,537

; PRIOR FILING DATE: 1997-05-17
; PRIOR APPLICATION NUMBER: US 60/061,684

; PRIOR FILING DATE: 1997-10-10
; NUMBER OF SEQ ID NOS: 53

; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2

; LENGTH: 439
; TYPE: PRT

; ORGANISM: Homo sapiens fgl2
US-09-442-143A-2

Query Match 100.0%; Score 88; DB 4; Length 439;
Best Local Similarity 100.0%; Pred. No. 1.2e-05;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DRYPSGNCGLYSSG 15
|||||:|||||:
Db 364 DRYPSGNCGLYSSG 378

RESULT 4

US-09-341-587-2
; Sequence 1, Application US/09341-587
; Patent No. 6346606

; GENERAL INFORMATION:
; APPLICANT: Mollenhauer, Jan

; APPLICANT: Mollenhauer, Jan
; TITLE OF INVENTION: Protein Containing an SRCR Domain

; FILE REFERENCE: 4121-108
; CURRENT APPLICATION NUMBER: US/09/341-587

; CURRENT FILING DATE: 1999-08-31
; EARLIER APPLICATION NUMBER: PCT/DE98/00096

; EARLIER FILING DATE: 1998-01-09
; NUMBER OF SEQ ID NOS: 12

; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1

; LENGTH: 666
; TYPE: PRT

; ORGANISM: Homo sapiens
US-09-341-587-1

Query Match 52.3%; Score 46; DB 4; Length 666;
Best Local Similarity 64.3%; Pred. No. 36;
Matches 9; Conservative 2; Mismatches 1; Indels 2; Gaps 1;

QY 4 PSNGCG--LYSSG 15
|||:|||||:
Db 183 PSSNCGGLFYASG 196

RESULT 5

US-09-341-587-3
; Sequence 1, Application US/09341-587
; Patent No. 6346606

; GENERAL INFORMATION:
; APPLICANT: Mollenhauer, Jan

; APPLICANT: Mollenhauer, Jan
; TITLE OF INVENTION: Protein Containing an SRCR Domain

; FILE REFERENCE: 4121-108
; CURRENT APPLICATION NUMBER: US/09/341-587

; CURRENT FILING DATE: 1999-08-31
; EARLIER APPLICATION NUMBER: PCT/DE98/00096

; EARLIER FILING DATE: 1998-01-09
; NUMBER OF SEQ ID NOS: 12

; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3

; LENGTH: 1785
; TYPE: PRT

; ORGANISM: Homo sapiens
US-09-341-587-3

Query Match 52.3%; Score 46; DB 4; Length 1785;
Best Local Similarity 64.3%; Pred. No. 98;
Matches 9; Conservative 2; Mismatches 1; Indels 2; Gaps 1;

QY 4 PSNGCG--LYSSG 15
|||:|||||:
Db 1134 PSSNCGGLFYASG 1147

RESULT 6

US-09-334-220-1
; Sequence 1, Application US/09334-220
; Patent No. 6323177

; GENERAL INFORMATION:
; APPLICANT: St. Jude's Children's Research Hospital

; APPLICANT: Curran, Thomas
; APPLICANT: D'Arcangelo, Gabriella

; TITLE OF INVENTION: INTERACTION OF REELIN WITH VERY LOW
; TITLE OF INVENTION: DENSITY LIPOPROTEIN (VLDL) RECEPTOR FOR SCREENING AND

; FILE REFERENCE: 2427/0704
; CURRENT APPLICATION NUMBER: US/09/334-220

; CURRENT FILING DATE: 1999-06-16
; NUMBER OF SEQ ID NOS: 5

; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1

; LENGTH: 3460
; TYPE: PRT

; ORGANISM: Homo sapien
US-09-334-220-1

Query Match 52.3%; Score 46; DB 4; Length 3460;
Best Local Similarity 71.4%; Pred. No. 1.9e+02;
Matches 10; Conservative 0; Mismatches 2; Indels 2; Gaps 1;

QY 3 YPSGNCGLY--YSS 14
|||:|||||:
Db 1973 YPGNGIGLYCPYSS 1986

RESULT 7

US-09-334-220-2
; Sequence 2, Application US/09334-220
; Patent No. 6323177

; GENERAL INFORMATION:
; APPLICANT: St. Jude's Children's Research Hospital

; APPLICANT: Curran, Thomas
; APPLICANT: D'Arcangelo, Gabriella

; TITLE OF INVENTION: INTERACTION OF REELIN WITH VERY LOW
; TITLE OF INVENTION: DENSITY LIPOPROTEIN (VLDL) RECEPTOR FOR SCREENING AND

; FILE REFERENCE: 2427/0704
; CURRENT APPLICATION NUMBER: US/09/334-220

; CURRENT FILING DATE: 1999-06-16
; NUMBER OF SEQ ID NOS: 5

; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1

; LENGTH: 3460
; TYPE: PRT

; ORGANISM: Homo sapien
US-09-334-220-1

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{
; FILE REFERENCE: 2427/0F704
; CURRENT APPLICATION NUMBER: US/09/334,220
; CURRENT FILING DATE: 1999-06-16
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 3461
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-334-220-2
Query Match      52.3%; Score 45; DB 4; Length 3461;
Best Local Similarity 71.4%; Pred. No. 1.9e+02;
Matches 10; Conservative 0; Mismatches 2; Indels 2; Gaps 1;

QY 3 YPSGNCGLY--YSS 14
      |||||
DB 1974 YPGNGIGLYCPYSS 1987

RESULT 8
US-09-198-452A-7
; Sequence 7, Application US/09198452A
; Patent No. 6559294
; GENERAL INFORMATION:
; APPLICANT: Grifais, R.
; TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragments
; TITLE OF INVENTION: thereof and uses thereof, in particular for the diagnosis, prevet
; TITLE OF INVENTION: and treatment of infection
; FILE REFERENCE: 9710-003-999
; CURRENT APPLICATION NUMBER: US/09/198,452A
; CURRENT FILING DATE: 1998-11-24
; NUMBER OF SEQ ID NOS: 6849
; SEQ ID NO 7
; LENGTH: 460
; TYPE: PRT
; ORGANISM: Chlamydia pneumoniae
US-09-198-452A-7
Query Match      48.9%; Score 43; DB 4; Length 460;
Best Local Similarity 60.0%; Pred. No. 70;
Matches 6; Conservative 1; Mismatches 3; Indels 3; Gaps 0;

QY 3 YPSGNCGLY 12
      |||||
DB 7 PPGNCNCY 16

RESULT 9
US-09-328-352-6858
; Sequence 6858, Application US/09328352
; Patent No. 6562958
; GENERAL INFORMATION:
; APPLICANT: Gary J. Breton et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
; TITLE OF INVENTION: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 67099-03PA
; CURRENT APPLICATION NUMBER: US/09/328,352
; CURRENT FILING DATE: 1999-06-04
; NUMBER OF SEQ ID NOS: 8252
; SEQ ID NO 6858
; LENGTH: 409
; TYPE: PRT
; ORGANISM: Acinetobacter baumannii
US-09-328-352-6858
Query Match      47.7%; Score 42; DB 4; Length 409;
Best Local Similarity 100.0%; Pred. No. 88;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 SGNCGLY 11
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DB 396 SGNCGLY 402
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RESULT 10
US-08-933-821-6
; Sequence 6, Application US/08933821
; Patent No. 5972338
; GENERAL INFORMATION:
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; TITLE OF INVENTION: Tie Ligands
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/933,821
; FILING DATE:
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Dreger, Ginger R.
; REGISTRATION NUMBER: 33,055
; REFERENCE/DOCKET NUMBER: P1130
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-3216
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 470 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
US-08-933-821-6
Query Match      47.2%; Score 41.5; DB 2; Length 470;
Best Local Similarity 60.0%; Pred. No. 1.2e+02;
Matches 9; Conservative 0; Mismatches 5; Indels 1; Gaps 1;

QY 1 DRYPSGNCGLYSSG 15
      |||||
DB 404 DSY-SGNCALYQRGG 417

RESULT 11
US-08-960-507-6
; Sequence 6, Application US/08960507
; Patent No. 6057435
; GENERAL INFORMATION:
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; TITLE OF INVENTION: Tie Ligands
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/960,507
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: FILING DATE:
: CLASSIFICATION: 516
: ATTORNEY/AGENT INFORMATION:
: NAME: Dreger, Ginger R.
: REGISTRATION NUMBER: 33,055
: REFERENCE/DOCKET NUMBER: P1130p1
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 650/225-3216
: TELEFAX: 650/952-9881
: INFORMATION FOR SEQ ID NO: 6:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 470 amino acids
: TYPE: Amino Acid
: TOPOLOGY: Linear
: US-08-960-507-6

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Query Match 47.2% Score 41.5; DB 3; Length 470;
Best Local Similarity 60.0%; Pred. No. 1.2e+02;
Matches 9; Conservative C; Mismatches 5; Indels 1; Gaps 1;

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QY 1 DRYPSGNCGLYSSG 15
| | | | | | |
Db 404 DSY-SGNCALYQRCG 417

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: RESULT 12
: US-09-136-828-6
: Sequence 6, Application US/09136828
: Patent No. 6350450
: GENERAL INFORMATION:
: APPLICANT: Godowski, Paul J.
: APPLICANT: Gurney, Austin L.
: TITLE OF INVENTION: Tie Ligands
: NUMBER OF SEQUENCES: 17
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Genentech, Inc.
: STREET: 1 DNA Way
: CITY: South San Francisco
: STATE: California
: COUNTRY: USA
: ZIP: 94080

```

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: COMPUTER READABLE FORM:
: MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: WinPatIn (Genentech)
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/09/136,828
: FILING DATE:
: CLASSIFICATION:

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: ATTORNEY/AGENT INFORMATION:
: NAME: Dreger, Ginger R.
: REGISTRATION NUMBER: 33,055
: REFERENCE/DOCKET NUMBER: P1130R1A
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 650/225-3216
: TELEFAX: 650/952-9881
: INFORMATION FOR SEQ ID NO: 6:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 470 amino acids
: TYPE: Amino Acid
: TOPOLOGY: Linear
: US-09-136-828-6

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Query Match 47.2% Score 41.5; DB 4; Length 470;
Best Local Similarity 60.0%; Pred. No. 1.2e+02;
Matches 9; Conservative 0; Mismatches 5; Indels 1; Gaps 1;

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QY 1 DRYPSGNCGLYSSG 15
| | | | | | |
Db 404 DSY-SGNCALYQRCG 417

```

```

: RESULT 13
: US-09-332-928A-6
: Sequence 6, Application US/09332928A
: Patent No. 6368853
: GENERAL INFORMATION:
: APPLICANT: Godowski, Paul J.
: APPLICANT: Gurney, Austin L.
: TITLE OF INVENTION: Tie Ligands
: NUMBER OF SEQUENCES: 17
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Genentech, Inc.
: STREET: 1 DNA Way
: CITY: South San Francisco
: STATE: California
: COUNTRY: USA
: ZIP: 94080
: COMPUTER READABLE FORM:
: MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: WinPatIn (Genentech)
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/09/332,928A
: FILING DATE: 14-Jun-1999
: CLASSIFICATION: <Unknown>
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: 08/933,821
: FILING DATE: <Unknown>
: ATTORNEY/AGENT INFORMATION:
: NAME: Dreger, Ginger R.
: REGISTRATION NUMBER: 33,055
: REFERENCE/DOCKET NUMBER: P113C
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 650/225-3216
: TELEFAX: 650/952-9881
: INFORMATION FOR SEQ ID NO: 6:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 470 amino acids
: TYPE: Amino Acid
: TOPOLOGY: Linear
: US-09-332-928A-6

```

```

Query Match 47.2% Score 41.5; DB 4; Length 470;
Best Local Similarity 60.0%; Pred. No. 1.2e+02;
Matches 9; Conservative C; Mismatches 5; Indels 1; Gaps 1;

```

```

QY 1 DRYPSGNCGLYSSG 15
| | | | | | |
Db 404 DSY-SGNCALYQRCG 417

```

```

: RESULT 14
: US-09-136-828-6
: Sequence 6, Application US/09136801
: Patent No. 6413770
: GENERAL INFORMATION:
: APPLICANT: Godowski, Paul J.
: APPLICANT: Gurney, Austin
: APPLICANT: Hillan, Kenneth
: APPLICANT: Botstein, David
: APPLICANT: Goddard, Audrey
: APPLICANT: Roy, Margaret
: APPLICANT: Ferrara, Napoleone
: APPLICANT: Tumas, Daniel
: APPLICANT: Schwall, Ralph
: TITLE OF INVENTION: Tie Ligand Homologues
: NUMBER OF SEQUENCES: 35
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Genentech, Inc.
: STREET: 1 DNA Way
: CITY: South San Francisco
: STATE: California

```

COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatIn (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/136,801
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Dreger, Ginger R.
REGISTRATION NUMBER: 33,055
REFERENCE/DOCKET NUMBER: P1130P2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-3216
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 470 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
US-09-136-801-6

Query Match 47.2%; Score 41.5; DB 4; Length 470;
Best Local Similarity 60.0%; Pred. No. 1.2e+02;
Matches 9; Conservative 0; Mismatches 5; Indels 1; Gaps 1;

QY 1 DRYPSGNCGLYYSSG 15
DB 404 DSY-SGNCALYQRGG 417

RESULT 15
US-09-332-929-6
Sequence 6, Application US/09332929
Patent No. 6420542
GENERAL INFORMATION:
APPLICANT: Godowski, Paul J.
APPLICANT: Gurney, Austin L.
TITLE OF INVENTION: Tie Ligands
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatIn (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/332,929
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/933,921
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Dreger, Ginger R.
REGISTRATION NUMBER: 33,055
REFERENCE/DOCKET NUMBER: P1130
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-3216
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 470 amino acids
TYPE: Amino Acid

TOPOLOGY: Linear
US-09-332-929-6
Query Match 47.2%; Score 41.5; DB 4; Length 470;
Best Local Similarity 60.0%; Pred. No. 1.2e+02;
Matches 9; Conservative 0; Mismatches 5; Indels 1; Gaps 1;
QY 1 DRYPSGNCGLYYSSG 15
DB 404 DSY-SGNCALYQRGG 417
Search completed: November 5, 2003, 16:49:00
Job time: 2.05727 secs

GenCore version 5.1.6
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CM protein - protein search, using sw model

Run on: November 5, 2003, 16:55:36; Search time 20 seconds
(without alignments)
72.127 Million cell updates/sec

Title: US-09-902-563-18

Perfect score: 88

Sequence: 1 DRYPSGNGLYSSG 15

Scoring table: BLOSUM62

Gapop 10.0, Gapext 0.5

Searched: 283308 seqs, 96168682 residues

Total number of hits satisfying chosen parameters: 2520

Minimum DB seq length: 0
Maximum DB seq length: 15

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database: PIR 75:
1: PIR1:
2: PIR2:
3: PIR3:
4: PIR4:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	31	35.2	14	A58963	alpha-conotoxin Cn
2	31	35.2	15	NTKXAG	alpha-conotoxin GI
3	26	29.5	15	PQ0017	terminal protein -
4	24	27.3	10	C41946	T-cell receptor ga
5	23.5	26.7	12	S25056	Ig heavy chain - m
6	23	26.1	10	PT0243	Ig heavy chain CRD
7	23	26.1	13	UTJG3	tremorogen a-13
8	23	26.1	14	PH3792	T-cell receptor al
9	23	26.1	15	PH1366	Ig heavy chain bu
10	23	26.1	15	PH0750	T-cell receptor be
11	23	26.1	15	PJ0110	complement factor
12	22.5	25.6	11	B41946	T-cell receptor Ga
13	22	25.0	9	S19329	sperm-activating p
14	22	25.0	11	PT3302	Ig heavy chain CRD
15	22	25.0	13	NTKX2G	alpha-conotoxin GI
16	22	25.0	13	I50173	alpha-2 collagen -
17	22	25.0	14	NTKX-M	alpha-conotoxin M-
18	22	25.0	14	PH1305	Ig heavy chain D7
19	22	25.0	15	C3765	hypothetical prote
20	21	23.9	9	PT0288	Ig heavy chain CRD
21	21	23.9	9	C41946	T-cell receptor ga
22	21	23.9	9	PQ0027	pev-tachykinin - p
23	21	23.9	10	B34887	T-cell receptor ga
24	21	23.9	11	PH1584	Ig H chain V-D-J r
25	21	23.9	12	H41946	T-cell receptor ga
26	21	23.9	13	A28953	alpha-conotoxin Gi
27	21	23.9	13	A51210	antibiotic GE2270
28	21	23.9	15	PT0085	protein QAC0027 -
29	21	23.9	15	S47387	T-cell antigen rec

30 21 23.9 15 2 S03955 acidic fibroblast
31 21 23.9 15 2 S08301 epidermal growth f
32 20 22.7 6 2 P10652 T-cell receptor be
33 20 22.7 11 2 S68637 acetylcholinestera
34 20 22.7 13 2 PH1596 Ig H chain V-D-J r
35 20 22.7 14 2 S58862 botulinum neurotox
36 20 22.7 14 2 S58862 botulinum neurotox
37 20 22.7 14 2 P10252 Ig heavy chain CRD
38 20 22.7 14 2 PH1597 Ig H chain V-D-J r
39 19 21.6 7 2 A11483 aspartate transami
40 19 21.6 10 2 A31571 hypertetralosemic/
41 19 21.6 12 2 S09082 proteasome chain 1
42 19 21.6 12 2 PH0802 T-cell receptor al
43 19 21.6 13 2 PH0788 T-cell receptor al
44 19 21.6 14 2 PA0109 porin por 1B - Ara
45 19 21.6 14 2 PA0045 porin por1 - Arabi

ALIGNMENTS

RESULT 1

A58963
M:Contains: alpha-conotoxin Cn1A - cone shell (Conus consors)
C:Species: Conus consors
C:Date: 16-Jul-1999 #sequence_revision: 16-Jul-1999 #text_change 16-Jul-1999
C:Accession: A58963
R:FAVreau, F.; Krimm, J.; Le Gall, F.; Bobenrieth, M.C.; Lanthanh, H.; Bouet, F.; Serv
Biochemistry 39, 6317-6326, 1999
A:Title: Biochemical characterization and nuclear magnetic resonance structure of nove
A:Reference number: A58963; MUID:99255390; PMID:10320362
A:Accession: A58963
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-14 <FAV>
C:Superfamily: alpha-conotoxin
C:Keywords: acetylcholine receptor inhibitor; amidated carboxyl end; postsynaptic neur
F:1-14/Product: alpha-conotoxin Cn1A #status experimental <NATA>
F:3-14/Product: alpha-conotoxin Cn1B #status experimental <NATA>
F:3-8,4-14/Disulfide bonds: #status experimental
F:14/Modified site: amidated carboxyl end (Cys) #status experimental

Query Match: 35.2% Score 31; DB 2; Length 14;
Best Local Similarity 83.3%; Pred. No. 1.1e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 8 CGLYYS 13
|||

Db 8 CGKYYS 13
|||

RESULT 2

NTKXAG
M:Alterrate Names: alpha-Ctx-G1A - cone shell (Conus geographus)
N:Contains: alpha-conotoxin Gi
C:Species: Conus geographus (geography cone)
C:Date: 24-Sep-1981 #sequence_revision 24-Sep-1981 #text_change 15-Sep-2000
C:Accession: A01782
R:Gray, W.R.; Lucque, A.; Olivera, B.M.; Barrett, J.; Cruz, L.J.
J. Biol. Chem. 256, 4734-4740, 1981
A:Title: Peptide toxins from Conus geographus venom.
A:Reference number: A92320; MUID:91191854; PMID:7014556
A:Accession: A01782
A:Molecule type: protein
A:Residues: 1-15 <GRA>
R:Gray, W.R.; Rivier, J.E.; Galyean, R.; Cruz, L.J.; Olivera, B.M.
J. Biol. Chem. 259, 12247-12251, 1983
A:Title: Conotoxin M1: disulfide bonding and conformational states.
A:Reference number: A92396; MUID:84032400; PMID:6630187
A:Contents: annotation; disulfide bonds
R:Guddat, L.W.; Shan, L.; Martin, J.L.; Edmundson, A.B.; Gray, W.R.

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submitted to the Brookhaven Protein Data Bank, May 1996
A:Reference number: A66253; PDB:INCT
A:Contents: annotation; X-ray crystallography, 1.2 angstroms, residues 1-13
R:Guddat, L.W.; Martin, C.A.; Shan, L.; Edmundson, A.B.; Gray, W.R.
Biochemistry 35, 11329-11335, 1996
A:Title: Three-dimensional structure of the alpha-conotoxin GI at 1.2 angstroms resolution
A:Reference number: A58592; MUID:96378624; PMID:8784187
A:Contents: annotation; X-ray crystallography, 1.2 angstroms
R:Pardi, A.; Galdes, A.; Florence, J.; Manicente, D.
Biochemistry 28, 5494-5501, 1989
A:Title: Solution structures of alpha-conotoxin GI determined by two-dimensional NMR spectroscopy
A:Reference number: A30629; MUID:89375269; PMID:2775719
A:Contents: annotation; conformation by (1)H-NMR
C:Comment: This alpha-conotoxin, as an acetylcholine receptor inhibitor, is a postsynaptic
C:Superfamily: alpha-conotoxin
C:Keywords: acetylcholine receptor inhibitor; amidated carboxyl end; blocked carboxyl end
F:1-15/Product: conotoxin GIA #status experimental <GIA>
F:1-13/Product: conotoxin GI #status experimental <GIC>
F:2-7-3-13/Disulfide bonds: #link GIA #status predicted
F:2-7-3-13/Disulfide bonds: #link GIC #status experimental
F:13/Modified site: amidated carboxyl end (Cys) (amide in mature form from following gly
F:13/Modified site: blocked carboxyl end (Lys) (probably amidated) #s-status experimental

Query Match          35.5%; Score 31; DB 1; Length 15;
Best Local Similarity 62.5%; Pred. No. 1.2e+02;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 8 CGLYYSSG 15
   ||| |||
Db 7 CGRYSCG 14

RESULT 3
PQ0017
Terminal protein - phase M2 (fragment)
C:Species: phase M2
C:Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 20-Sep-1999
C:Accession: PQ0017
R:Matsumoto, K.; Takano, H.; Kim, C.I.; Hirokawa, H.
Gene 84, 247-255, 1989
A:Title: Primary structure of bacteriophage M2 DNA polymerase: conserved segments within
A:Reference number: PQ0161; MUID:90128268; PMID:2515115
A:Accession: PQ0017
A:Molecule type: DNA
A:Residues: 1-15 <MA>
A:CROSS-references: G3:M33144; NID:G215507; PIDN:AA032367.1; PID:G215503
C:Genetics:
A:Gene: E
C:Superfamily: phage PZA terminal protein

Query Match          29.5%; Score 26; DB 2; Length 15;
Best Local Similarity 50.0%; Pred. No. 7.3e+02;
Matches 5; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 DRYRGDVL 10
   ||| |
Db 1 DRYRGDVL 10

RESULT 4
C41946
T-cell receptor gamma chain (1t.60; - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 07-May-1999
C:Accession: C41946
R:Whetzel, M.; Mostey, R.L.; Whetzel, L.; Schaefer, F.V.; Miller, K.S.; Klein, J.R.
Mol. Cell. Biol. 11, 5902-5909, 1991
A:Title: Rearrangement and junctional-site sequence analyses of T-cell receptor gamma ge
A:Reference number: A41946; MUID:92049316; PMID:1858619
A:Accession: C41946
A:Status: preliminary; not compared with conceptual translation
A:Molecule type: DNA
A:Residues: 1-10 <WHE>

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C:Keywords: T-cell receptor

Query Match          27.3%; Score 24; DB 2; Length 10;
Best Local Similarity 50.0%; Pred. No. 1e+03;
Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 8 GGLYYSSG 15
   ||| |||
Db 2 CAVWSGG 9

RESULT 5
S25056
Ig heavy chain - mouse
C:Species: Mus musculus (house mouse)
C:Date: 25-Feb-1994 #sequence_revision 01-Dec-1995 #text_change 20-Jun-2000
C:Accession: S25056
R:Jacob, J.; Kelsoe, G.
submitted to the EMBL Data Library, July 1992
A:Description: In situ studies on the primary immune response to (4-hydroxy-3-nitrophen
A:Reference number: S25024
A:Accession: S25056
A:Status: preliminary
A:Molecule type: nucleic acid
A:Residues: 1-12 <JAC>
A:CROSS-references: EMBL:X67386; NID:950927; PIDN:CAA47798.1; PID:G1333920
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin

Query Match          26.7%; Score 23.5; DB 2; Length 12;
Best Local Similarity 46.2%; Pred. No. 1.5e+03;
Matches 6; Conservative 0; Mismatches 2; Indels 5; Gaps 1;

QY 2 RYPSGNCGLYYSS 14
   ||| |||
Db 2 RYP-----YYGS 9

RESULT 6
PT0243
IG heavy chain CDR3 region (clone 2-103A) - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Aug-1996
C:Accession: PT0243
R:Yanada, M.; Wasserman, R.; Reichard, B.A.; Shane, S.; Caton, A.C.; Rovera, G.
J. Exp. Med. 173, 395-407, 1991
A:Title: Preferential utilization of specific immunoglobulin heavy chain diversity and
A:Reference number: PT0222; MUID:9110337; PMID:1899102
A:Accession: PT0243
A:Molecule type: DNA
A:Residues: 1-10 <YAM>
A:Experimental source: B lymphocyte
C:Keywords: heterotetramer; immunoglobulin

Query Match          26.1%; Score 23; DB 2; Length 10;
Best Local Similarity 71.4%; Pred. No. 1.5e+03;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 9 GJYYSSG 15
   ||| |||
Db 2 GJYDSSG 8

RESULT 7
JTCG3
Tremorogen a-13 - jelly fungus (Tremella mesenterica)
C:Species: Tremella mesenterica
C:Date: 03-Aug-1984 #sequence_revision 03-Aug-1984 #text_change 07-Nov-1997
C:Accession: A01641
R:Sakagami, Y.; Yoshida, M.; Isogai, A.; Suzuki, A.
Science 212, 1525-1527, 1981
A:Title: Peptide sex hormones inducing conjugation tube formation in compatible mating
A:Reference number: A94256

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A:Accession: A01641
A:Molecule type: protein
A:Residues: 1-13 <SAK>
C:Comment: Tremorgen a-13 is produced by the a mating-type cells and induces formation
C:Superfamily: tremorgen a-13
C:Keywords: extracellular protein; hormone; lipoprotein; pheromone; prenylated cysteine
F:13/Binding site: farnesyl (Cys); (covalent); #status experimental
F:13/Modified site: methyl ester carboxyl end (Cys) #status absent

Query Match      26.1%; Score 23; DB 1; Length 13;
Best Local Similarity 80.0%; Pred. No. 1.9e+03;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      4 PSQNC 8
DB      9 PSQVC 13

RESULT 8
T-cell receptor alpha chain (H2 V-alpha-2.7A.9) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997
C:Accession: PH0792
R:Casanova, J.L.; Romero, P.; Widmann, C.; Kourilsky, P.; Maryanski, J.L.
J. Exp. Med. 174, 1371-1383, 1991
A:Title: T cell receptor genes in a series of class I major histocompatibility complex-
allelic exclusion and antigen-specific repertoire.
A:Reference number: PH0746; MUID:92078846; PMID:1836010
A:Accession: PH0792
A:Molecule type: mRNA
A:Residues: 1-14 <CAS>
A:Cross-references: EMBL:X50897
A:Experimental source: T lymphocyte
C:Keywords: T-cell receptor

Query Match      26.1%; Score 23; DB 2; Length 14;
Best Local Similarity 45.5%; Pred. No. 2.1e+03;
Matches 5; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY      5 SGNCGLYSSG 15
DB      4 SANSCTYQREG 14

RESULT 9
IG heavy chain DJ region (clone C11-106) - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 07-May-1999
C:Accession: PH1366
R:Wasserman, R.; Galili, N.; Ito, Y.; Reichard, B.A.; Shano, S.; Rovera, G.
J. Exp. Med. 176, 1577-1591, 1992
A:Title: Predominance of fetal type DJH joining in young children with B precursor lymphoma
A:Reference number: PH1302; MUID:93094761; PMID:1463419
A:Accession: PH1366
A:Molecule type: DNA
A:Residues: 1-15 <WAS>
C:Keywords: heterotetramer; immunoglobulin

Query Match      26.1%; Score 23; DB 2; Length 15;
Best Local Similarity 45.5%; Pred. No. 2.2e+03;
Matches 5; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY      5 SGNCGLYSSG 15
DB      4 SGYGVGVWGGQ 14

RESULT 10
PH0750
T-cell receptor beta chain (CII) - mouse (fragment)
C:Species: Mus musculus (house mouse)

C:Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997
C:Accession: PH0750
R:Casanova, J.L.; Romero, P.; Widmann, C.; Kourilsky, P.; Maryanski, J.L.
J. Exp. Med. 174, 1371-1383, 1991
A:Title: T cell receptor genes in a series of class I major histocompatibility complex
allelic exclusion and antigen-specific repertoire
A:Reference number: PH0746; MUID:92078846; PMID:1836010
A:Accession: PH0750
A:Molecule type: mRNA
A:Residues: 1-15 <CAS>
A:Cross-references: EMBL:X0684;
A:Experimental source: T lymphocyte
C:Keywords: T-cell receptor

Query Match      26.1%; Score 23; DB 2; Length 15;
Best Local Similarity 44.4%; Pred. No. 2.2e+03;
Matches 4; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY      4 PSQNCGLYY 12
DB      5 PSANTGQLY 13

RESULT 11
EL0110
Complement factor B1-Bb and B2-Bb - guinea pig (fragment)
C:Species: Cavia porcellus (guinea pig)
C:Date: 31-Mar-1990 #sequence_revision 31-Mar-1990 #text_change 15-Nov-1996
C:Accession: PLO110
R:Matsumita, M.; Okada, H.
Yol Immunol. 26, 669-676, 1989
A:Title: Two forms of guinea pig factor B of the alternative complement pathway with d
A:Reference number: A93136; MUID:9384686; PMID:2779589
A:Accession: PLO110
A:Molecule type: protein
A:Residues: 1-15 <MAT>
C:Keywords: complement alternate pathway; glycoprotein

Query Match      26.1%; Score 23; DB 2; Length 15;
Best Local Similarity 37.5%; Pred. No. 2.2e+03;
Matches 3; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY      4 PSQNCGLYY 11
DB      6 PAGSMXNY 13

RESULT 12
B41946
T-cell receptor gamma chain (it.57) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 07-May-1999
C:Accession: B41946
R:Whetsell, V.; Mosley, R.L.; Whetsell, L.; Schaefer, F.V.; Miller, K.S.; Klein, J.R.
Mol. Cell. Biol. 11, 5902-5909, 1991
A:Title: Rearrangement and junctional-site sequence analyses of T-cell receptor gamma
A:Reference number: A41946; MUID:92049316; PMID:1658619
A:Accession: B41946
A:Status: preliminary; not compared with conceptual translation
A:Molecule type: DNA
A:Residues: 1-11 <WHE>
C:Keywords: T-cell receptor

Query Match      25.6%; Score 22.5; DB 2; Length 11;
Best Local Similarity 55.6%; Pred. No. 2e+03;
Matches 5; Conservative 2; Mismatches 1; Indels 1; Gaps 1;

QY      8 CGLY-YSSG 15
DB      2 CAVWRYSSG 10

RESULT 13

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S19329

sparm-activating peptide SAp - sea urchin (Stomopneustes variolus)

C:Species: Stomopneustes variolus

C:Date: 04-Dec-1992 #sequence_revision 04-Dec-1992 #text_change 18-Aug-2000

C:Accession: S19329

R:Yoshino, K.; Takao, T.; Shimonishi, Y.; Suzuki, N.

FEBS Lett. 294, 179-182, 1991

A:Title: Determination of the amino acid sequence of an intramolecular disulfide linkage

A:Reference number: S19329; MUID:92097763; PMID:1756859

A:Accession: S19329

A:Molecule type: protein

A:Residues: 1-9 <YOS>

C:Superfamily: unassigned animal peptides

F:3-8/Disulfide bonds: #status predicted

Query Match 25.0%; Score 22; DB 2; Length 9;

Best Local Similarity 60.0%; Pred. No. 2.8e+05;

Matches 3; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 4 PSGNC 8

Db 4 PEGKC 8

RESULT 14

PT0302

IG heavy chain CRD3 region (clone 5-112) - human (fragment)

C:Species: Homo sapiens (man)

C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Aug-1996

C:Accession: PT0302

R:Yamada, Y.; Wasserman, R.; Reichard, B.A.; Shane, S.; Caton, A.J.; Rovera, G.

J. Exp. Med. 173, 395-407, 1991

A:Title: Preferential utilization of specific immunoglobulin heavy chain diversity and

A:Reference number: PT0222; MUID:91108337; PMID:1699402

A:Accession: PT0302

A:Molecule type: DNA

A:Residues: 1-11 <YAM>

A:Experimental source: B lymphocyte

C:Keywords: heterotetramer; immunoglobulin

Query Match 25.0%; Score 22; DB 2; Length 11;

Best Local Similarity 71.4%; Pred. No. 2.4e+03;

Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 9 GJYSSG 15

Db 3 GRYSSG 9

RESULT 15

NTKX2G

alpha-conotoxin GII - cone shell (Conus geographus)

C:Species: Conus geographus (geography cone)

C:Date: 24-Sep-1981 #sequence_revision 24-Sep-1981 #text_change 23-May-1997

C:Accession: A01783

R:Gray, W.R.; Luque, A.; Olivera, B.M.; Barrett, J.; Cruz, L.J.

J. Biol. Chem. 256, 4734-4740, 1981

A:Title: Peptide toxins from Conus geographus venom.

A:Reference number: A92396; MUID:81191854; PMID:704556

A:Accession: A01783

A:Molecule type: protein

A:Residues: 1-13 <GRA>

R:Gray, W.R.; Rivier, J.E.; Galyean, R.; Cruz, L.J.; Olivera, B.M.

J. Biol. Chem. 258, 12247-12251, 1983

A:Title: Conotoxin MI. Disulfide bonding and conformational states.

A:Reference number: A92396; MUID:8403400; PMID:6630187

A:Contents: annotation; disulfide bonds

C:Comment: This alpha-conotoxin, as an acetylcholine receptor inhibitor, is a postsynaptic

C:Superfamily: alpha-conotoxin

C:Keywords: acetylcholine receptor inhibitor; blocked carboxyl end; postsynaptic neuroto

F:2-7,3-13/Disulfide bonds: #status predicted

F:13/Modified site: blocked carboxyl end (Cys) (probably amidated) #status experimental

Query Match 25.0%; Score 22; DB 1; Length 13;

Best Local Similarity 50.0%; Pred. No. 2.8e+03;

Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 8 CGLYYS 13

Db 7 CGKHS 12

Search completed: November 5, 2003, 16:59:09

Job time : 22 secs

GenCore version 5.1.1.6
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OM protein - protein search, using sw model

Run on: November 5, 2003, 16:49:10 : Search time 11 seconds
(without alignments)
64,127 Million cell updates/sec

Title: US-09-902-563-18

Perfect score: 99

Sequence: 1 DRYPSGNCLLYSSG 15

Scoring table:

BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 795

Minimum DB seq length: 0

Maximum DB seq length: 15

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_41.4

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	31	35.2	14	1	CXAL_CONCN
2	31	35.2	15	1	CXAL_CONGE
3	26	29.5	15	1	TERV_BPM2
4	23	26.1	13	1	TALV_TREME
5	23	26.1	14	1	MARI_AITSP
6	23	26.1	15	1	UC14_MAIZE
7	22	25.0	9	1	SAP_STOVA
8	22	25.0	13	1	CXAL_CONGE
9	22	25.0	14	1	CXAL_CONNA
10	21	23.9	9	1	TRP4_LEUMA
11	21	23.9	15	1	CIQA_RAT
12	21	23.9	15	1	EGFI_CANFA
13	20	22.7	10	1	PCPK_FASHE
14	19	21.6	9	1	TKLI_LOCMI
15	19	21.6	10	1	HTF_HELZE
16	19	21.6	14	1	SCK3_LEIQU
17	19	21.6	15	1	TAL_TREBR
18	19	21.6	15	1	UC05_MAIZE
19	18	20.5	10	1	AMPN_HELAM
20	18	20.5	13	1	URAI_HUMAN
21	18	20.5	14	1	CAT2_FASHE
22	18	20.5	14	1	HV14_PIG
23	16	20.5	14	1	LPER_BACLI
24	16	20.5	15	1	KLOM_LUNTE
25	18	20.5	15	1	UC19_MAIZE
26	17	19.3	8	1	ALLI_CYDPO
27	17	19.3	8	1	LCK9_LEUMA
28	17	19.3	9	1	OXVA_SQUAC
29	17	19.3	9	1	CKYT_RABIT
30	17	19.3	10	1	FARS_MACRS
31	17	19.3	12	1	CXAL_CONNR
32	17	19.3	14	1	SCDN_STRGR
33	17	19.3	15	1	OBPA_MAMBR

34	16	18.2	8	1	ALL6_CVDPO
35	16	18.2	9	1	COW_CONVE
36	16	18.2	10	1	COXO_THUOB
37	16	18.2	10	1	CU30_LOCMI
38	16	18.2	11	1	CORZ_PERAM
39	16	18.2	11	1	EPG_CLOPA
40	16	18.2	12	1	FARI_CALVO
41	16	18.2	12	1	FRI_SARBU
42	16	18.2	12	1	FRI_LITIN
43	16	18.2	12	1	LICH_BACLI
44	16	18.2	12	1	RFL_CONSP
45	16	18.2	13	1	LPAA_PORGI

ALIGNMENTS

RESULT 1
CXAL_CONCN STANDARD; PRF; 14 AA.
AC P56973;
DE 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DE 28-FEB-2003 (Rel. 41, Last annotation update)
DE Alpha-conotoxin CN1A (Contains: Alpha-conotoxin CN1B)
CS Conus consors (Single cone)
CC Apokaryota; Metazoa; Mollusca; Gastropoda; Orthogastropoda;
CC Apogastropoda; Caenogastropoda; Soiteoconcha; Hypsogastropoda;
CC Neogastropoda; Conoidea; Conidae; Conus.
OC NCB TaxID=101297;
RN 11
RP SEQUENCE, SYNTHESIS, CHARACTERIZATION, AND STRUCTURE BY NMR.
RC TISSUE=Venom;
RX MEDLINE=9255390; PubMed=10320362;
RA Favreau P., Krimm I., le Gall F., Bobenrieth M.J., Lamthanh H.,
RA Bouet F., Servent D., Molgo J., Menez A., Letourneux Y.,
RA Lancelin J.-M.
RT "Biochemical characterization and nuclear magnetic resonance
structure of novel alpha-conotoxins isolated from the venom of Conus
consors.";
RL Biochemistry 38:6317-6326(1999).
CC -!- FUNCTION: ALPHA-CONOTOXINS ACT ON POSTSYNAPTIC MEMBRANES, THEY
BIND TO THE NICOTINIC ACETYLCHOLINE RECEPTORS (NACHR) AND THUS
INHIBIT THEM. THIS PEPTIDE SEEMS TO BE A POTENT AND SELECTIVE
BLOCKER OF MUSCULAR SUBTYPE OF NACHR.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Expressed by the venom duct.
CC -!- SIMILARITY: BELONGS TO THE A-SUPERFAMILY OF CONOTOXINS. ALPHA-TYPE
FAMILY.
DR PIR: A58963; A58963.
DR PDB: 1B45; 09-JUL-99.
KW Postsynaptic neurotoxin; Neurotoxin; Toxin;
KW Acetylcholine receptor inhibitor; Amidation; 3D-structure.
FT PEPTIDE 1 14 ALPHA-CONOTOXIN CN1A.
FT PEPTIDE 3 14 ALPHA-CONOTOXIN CN1B.
FT DISULFID 3 8
FT DISULFID 4 14
FT MOD_RES 14 14 AMIDATION.
FT HELIX 6 8
FT TURN 9 10
SQ SEQUENCE 14 AA; 1548 KW; DEEE919699F5E5BD CRC64;
Query Match 35.2%; Score 31; DB 1; Length 14;
Best Local Similarity 83.3%; Pred. No. 35;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

CY 8 CGJYYS 13

DB 8 CGJYYS 13

RESULT 2

CXAL_CONGE


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TERM: BPV2
ID TERM_BPM2 STANDARD; PRT; 15 AA.
AC P19897;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE DNA terminal protein (Protein GP3) (Fragment);
GN 3 OR E.
OS Bacteriophage M2.
CC Viruses; dsDNA viruses, no RNA stage; Caudovirales; Podoviridae;
CC phi-29-like viruses.
OX NCBI_TaxID=10751;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=90128268; PubMed=255115;
RA Matsumoto K., Takano H., Kim C.I., Hirokawa H.;
RT "Primary structure of bacteriophage M2 DNA polymerase: conserved
RT segments within protein-priming DNA polymerases and DNA polymerase I
RT of Escherichia coli.";
RL Gene 84:247-255(1989).
CC -!- FUNCTION: DNA TERMINAL PROTEIN IS LINKED TO THE 5' ENDS OF
CC BOTH STRANDS OF THE GENOME THROUGH A PHOSPHODIESTER BOND BETWEEN
CC THE BETA-HYDROXYL GROUP OF A SERINE RESIDUE AND THE 5'-PHOSPHATE
CC OF THE TERMINAL DEOXYADENYLATE. THIS PROTEIN IS ESSENTIAL FOR DNA
CC REPLICATION AND IS INVOLVED IN THE PRIMING OF DNA ELONGATION.
CC
CC THIS SWISS-PROT entry is copyrighted. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
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CC or send an email to license@sib-sib.ch).
CC
CC -----
DR EMBL; M33144; AAA32367.1; -
DR PIR; PQ0017;
KW Early protein; DNA replication; DNA priming;
KW Covalent protein-DNA linkage.
FT NON_TER 1 1
FT SITE 5 7 CELL ATTACHMENT SITE (POTENTIAL).
SQ SEQUENCE 15 AA; 1797 MW; D3CBADF8759DEA36 CRC64;
Query Match 29.5%; Score 26; DB 1; Length 15;
Best Local Similarity 50.0%; Pred. No. 2.4e+02;
Matches 5; Conservative 1; Mismatches 4; Indels 0; Gaps 0;
QY 1 DRYPSGNGL 10
DB 1 DRYERGDNV 10
RESULT 4
TA13 TREME STANDARD; PRT; 13 AA.
AC P01370;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 01-NOV-1991 (Rel. 20, Last annotation update)
DE Tremorgen A-13.
OS Tremella mesenterica (Celly fungus).
CC Eukaryota; Fungi; Basidiomycota; Hymenomycetes; Heterobasidiomycetes;
CC Tremellorhizales; Tremellales; Tremellaceae; Tremella.
OX NCBI_TaxID=5217;
RN [1]
RP SEQUENCE.
RA Sakagami Y., Yoshida M., Isogai A., Suzuki A.;
RT "Peptide sex hormones inducing conjugation tube formation in
RT compatible mating-type cells of Tremella mesenterica.";
RL Science 212:1525-1527(1981)
CC -!- FUNCTION: TREMERGEN A-13 IS PRODUCED BY THE A MATING-TYPE CELLS.
CC AND INDUCES FORMATION OF CONJUGATION TUBES IN A MATING-TYPE CELLS.
DR PIR; A01644; JTG33.
KW Lipoprotein; Prenylation; Pheromone.
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FT LIPID 13 13 FARNESYL.
SQ SEQUENCE 13 AA; 1204 MW; 680304A9697BA864 CRC64;
Query Match 26.1%; Score 23; DB 1; Length 13;
Best Local Similarity 80.0%; Pred. No. 6.3e+02;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 4 PSGNC 8
DB 9 PSGVC 13
RESULT 5
MARI_ALTPS STANDARD; PRT; 14 AA.
ID MARI_ALTPS STANDARD; PRT; 14 AA.
AC P29399;
DT 01-DEC-1992 (Rel. 24, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Marinostatin C-2 [Marinostatin C-1; Marinostatin D].
OS Alteromonas sp. (Strain B-10-31).
CC Bacteria; Proteobacteria; Gammaproteobacteria; Alteromonadales;
CC Alteromonadaceae; Alteromonas.
OX NCBI_TaxID=29456;
RN [1]
RP SEQUENCE AND ACTIVE SITE.
RX MEDLINE=92176155; PubMed=1794974;
RA Takano R., Imada C., Kami K., Hara S.;
RT "The relative site of marinostatin, a proteinase inhibitor from
RT marine Alteromonas sp. B-10-31.";
RL J. Biochem. 110:856-858(1991).
CC -!- FUNCTION: INHIBITS SUBSTITUISIN, CHYMOTRYPSIN, AND ELASTASE, BUT
CC NOT TRYPSIN.
KW Serine protease inhibitor; Pyrrolidone carboxylic acid.
FT PEPTIDE 1 14
FT PEPTIDE 3 14 MARINOSTATIN C-2.
FT PEPTIDE 4 14 MARINOSTATIN C-1.
FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
FT ACT_SITE 6 7 REACTIVE BOND.
SQ SEQUENCE 14 AA; 1644 MW; 6E7CEE92EF32E44 CRC64;
Query Match 26.1%; Score 23; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 6.7e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2 RYPS 5
DB 7 RYPS 10
RESULT 6
UC14_MAIZE STANDARD; PRT; 15 AA.
ID UC14_MAIZE STANDARD; PRT; 15 AA.
AC P80620;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 25-JUL-1999 (Rel. 38, Last annotation update)
DE Unknown: protein from 2D-Page of etiolated coleoptile (Spot 258)
DE (fragment).
OS Zea mays (Maize).
CC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
CC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
CC PACCAD clade; Panicoideae; Andropogoneae; Zea.
OX NCBI_TaxID=4577;
RN [1]
RP SEQUENCE.
RC TISSUE=Coleoptile;
RA Touzet P., Riccardi F., Morin C., Damerval C., Huet J.-C.,
RA Pernollet J.-C., Zivy M., de Vienne D.;
RT "The maize two dimensional gel protein database: towards an integrated
RT genome analysis program.";
RL Theor. Appl. Genet. 91:997-1005(1996).
CC -!- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN
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CC PROTEIN IS: 5.9, ITS MW IS: 34.6 kDa.
DR Maize-2DPAGE; P80620; COLLECTIBLE.
DR MaizeDB; 123944; -.
FT NON_TER 1
FT NON_TER 15
SQ SEQUENCE 15 AA; 1564 MW; CFEBAACB7DE6658 CRC64;

Query Match: 26.1%; Score 23; DB 1; Length 15;
Best Local Similarity 57.1%; Pred. No. 7.2e+02;
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 6 GNGGLY 12
DB 4 GGGAY 10

RESULT 7
SAP_STOVA STANDARD; PRT; 9 AA.
ID SAP_STOVA STANDARD; PRT; 9 AA.
AC 24047;
DT 01-MAR-1992 (Rel. 21, Created)
DT 01-MAR-1992 (Rel. 21, Last sequence update)
DT 01-MAR-1992 (Rel. 21, Last annotation update)
DE Sperm-activating peptide (SAP).
OS Stomopneustes variolaris (Sea urchin).
OC Eukaryota; Metazoa; Echinodermata; Eleutherozoa; Echinozoa;
OC Echinoida; Euechinoida; Diadematacea; Phrynosomatoidea; Stomechinidae;
OC Stomopneustes.
OX NCBI_TaxID=7663;
RN [1]
RP SEQUENCE, AND DISULFIDE BOND.
RC TISSUE=Egg jelly; PubMed=758358.
RX MEDLINE=92097753;
RA Yoshino K.-I., Takao T., Shimomichi Y., Suzuki N.;
RT "Determination of the amino acid sequence of an intramolecular
RT disulfide linkage-containing sperm-activating peptide by tandem mass
RT spectrometry."
RL FEBS Lett. 294:179-182(1991).
CC -!- FUNCTION: CAUSE STIMULATION OF SPERM RESPIRATION AND MOTILITY
CC THROUGH INTRACELLULAR ALKALINIZATION, TRANSIENT ELEVATIONS OF
CC CAMP, CGMP AND CALCIUM LEVELS IN SPERM CELLS, AND TRANSIENT
CC ACTIVATION AND SUBSEQUENT INACTIVATION OF THE MEMBRANE FORM OF
CC GUANYLATE CYCLASE.
FT DISULFID 3
SQ SEQUENCE 9 AA; 1010 MW; C469B337B076EB9 CRC64;

Query Match 25.0%; Score 22; DB 1; Length 9;
Best Local Similarity 60.0%; Pred. No. 1.3e+05;
Matches 3; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4 PSNGC 8
DB 4 PEGKC 8

RESULT 8
CXA2_CONGE STANDARD; PRT; 13 AA.
ID CXA2_CONGE STANDARD; PRT; 13 AA.
AC P01520;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Alpha-conotoxin GI2.
OS Conus geographus (Geography cone).
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Orthogastropoda;
OC Apogastropoda; Caenogastropoda; Sorbeoconcha; Hypsogastropoda;
OC Neogastropoda; Conoidea; Conidae; Conus.
OX NCBI_TaxID=6491;
RN [1]
RP SEQUENCE.
RX MEDLINE=81a9:854; PubMed=7014556;
RA Gray W.R., Luque A., Olivera B.M., Barrett J., Cruz L.J.;
RT "Peptide toxins from Conus geographus venom.";
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RJ J. Biol. Chem. 256:4734-4740(1981).
RK [2]
RP DISULFIDE BONDS.
RX MEDLINE=94280842; PubMed=6466616;
RA Gray W.R., Luque F.A., Galyean R., Atherton E., Sheppard R.C.,
RA Stone E.L., Reyes A., Alford J., McIntosh M., Olivera B.M.,
RA Cruz L.J., Rivier J.;
RA "Conotoxin GI: disulfide bridges, synthesis, and preparation of
RT iodinated derivatives."
RJ Biochemistry 23:2796-2802(1984).
CC -!- FUNCTION: Alpha-conotoxins act on postsynaptic membranes, they
CC bind to the nicotinic acetylcholine receptors (nAChR) and thus
CC inhibit them.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Expressed by the venom duct.
CC -!- SIMILARITY: BELONGS TO THE A-SUPERFAMILY OF CONOTOXINS. ALPHA-TYPE
CC FAMILY.
DR PIR; A01783; NTKN2G.
DR HSSP; P56973; I845.
KW Postsynaptic neurotoxin; Neurotoxin; Toxin;
KW Acetylcholine receptor inhibitor; Amidation.
FT DISULFID 2 7
FT DISULFID 3 13
FT MOD_RES 13 13
SQ SEQUENCE 13 AA; 1422 MW; DEE831C39297EBD CRC64;

Query Match 25.0%; Score 22; DB 1; Length 13;
Best Local Similarity 50.0%; Pred. No. 9.1e+02;
Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 8 CGLYYS 13
DB 7 CGKPS 12

RESULT 9
CXA1_CONMA STANDARD; PRT; 14 AA.
ID CXA1_CONMA STANDARD; PRT; 14 AA.
AC P01521;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Alpha-conotoxin MI (M1).
OS Conus magus (Magus cone).
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Orthogastropoda;
OC Apogastropoda; Caenogastropoda; Sorbeoconcha; Hypsogastropoda;
OC Neogastropoda; Conoidea; Conidae; Conus.
OX NCBI_TaxID=6492;
RN [1]
RP SEQUENCE.
RX MEDLINE=81073458; PubMed=7149738;
RA McIntosh J.M., Cruz L.J., Hunkapiller M.W., Gray W.R., Olivera B.M.;
RT "Isolation and structure of a peptide toxin from the marine snail
RT Conus magus."
RJ Arch. Biochem. Biophys. 218:329-334(1982).
RK [2]
RP DISULFIDE BONDS.
RX MEDLINE=94032400; PubMed=66310187;
RA Gray W.R., Rivier J.E., Galyean R., Cruz L.J., Olivera B.M.;
RT "Conotoxin MI. Disulfide bonding and conformational states."
RJ J. Biol. Chem. 258:12247-12251(1983).
CC -!- FUNCTION: ALPHA-CONOTOXINS ACT ON POSTSYNAPTIC MEMBRANES, THEY
CC BIND TO THE NICOTINIC ACETYLCHOLINE RECEPTORS (NACHR) AND THUS
CC INHIBIT THEM.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Expressed by the venom duct.
CC -!- SIMILARITY: BELONGS TO THE A-SUPERFAMILY OF CONOTOXINS. ALPHA-TYPE
CC FAMILY.
DR PIR; A01784; NTKN1M.
DR HSSP; P56973; I845.
KW Postsynaptic neurotoxin; Neurotoxin; Toxin;
KW Acetylcholine receptor inhibitor; Amidation.
FT DISULFID 3 8
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FT DISULFID 4 14
FT MOD RES 14 14 AMINATION
SQ SEQUENCE 14 AA; 1499 MW; DEEE9198BF5E5SD CRC64;

Query Match 25.0%; Score 22; DB 1; Length 14;
Best Local Similarity 66.7%; Pred. No. 9.8e+02;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

CY 8 CGLYS 13
DB 8 CGKYS 13

RESULT 10
TRP4_LEUMA STANDARD; PRT; 9 AA.
ID TRP4_LEUMA
AC P81736;
DT 30-MAY-2003 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Tachykinin-related peptide 4 (IleuTRP 4).
CS Leucophaea maderae (Maderia cockroach).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pserygota;
OC Neoptera; Orthopteroidea; Dictyoptera; Blattaria; Blaberidae;
OC Blaberidae; Leucophaea.
OX NCBI_TaxID=6988;
RN [1]
PP SEQUENCE.
RC TISSUE=Midgut;
RX MEDLINE=97353012; PubMed=8897641;
Muren J.E., Naessel D.R.;
RT "Isolation of five tachykinin-related peptides from the midgut of
R. the cockroach Leucophaea maderae: existence of N-terminally extended
R. isoforms.";
RL Regui. Pept. 65:185-196(1996).
CC -!- FUNCTION: MYOACTIVE PEPTIDE. INCREASES THE AMPLITUDE AND FREQUENCY
OF SPONTANEOUS CONTRACTIONS AND TONUS OF HINDGUT MUSCLE.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: MIDGUT.
CC -!- SIMILARITY: SOME SIMILARITY TO TACHYKININS.
KW Tachykinin; Neuropeptide; Amidation.
FT MOD RES 9
SQ SEQUENCE 9 AA; 953 MW; 2403987699C865A7 CRC64;

Query Match 23.9%; Score 21; DB 1; Length 9;
Best Local Similarity 57.1%; Pred. No. 1.3e+05;
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

CY 4 PSNGNGL 10
DB 2 PSNGFMG 8

RESULT 11
C10A_RAT STANDARD; PRT; 15 AA.
ID C10A_RAT
AC P81729;
DT 01-JUL-1993 (Rel. 26, Created)
DT 01-JUL-1993 (Rel. 26, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Complement C1q subcomponent, A chain (fragment).
GN C10A.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
PP SEQUENCE.
RX MEDLINE=93218657; PubMed=9464426;
Wing M.G., Seilly D.J., Bridgman D.J., Harrison R.A.;
RT "Rapid isolation and biochemical characterization of rat C1 and C1q.";
RL Mol. Immunol. 30:433-440(1993).
CC -!- FUNCTION: C1Q ASSOCIATES WITH THE PROENZYME C1R AND C1S TO YIELD

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CC C1, THE FIRST COMPONENT OF THE SERUM COMPLEMENT SYSTEM. THE
CC COLLAGEN-LIKE REGIONS OF C1Q INTERACT WITH THE CA(2+)-DEPENDENT
CC C1R(2)C1S(2) PROENZYME COMPLEX, AND EFFICIENT ACTIVATION OF C1
CC TAKES PLACE ON INTERACTION OF THE GLOBULAR HEADS OF C1Q WITH THE
CC FC REGIONS OF IGG OR IGM ANTIBODY PRESENT IN IMMUNE COMPLEXES.
CC -!- SUBUNIT: C1 IS A CALCIUM-DEPENDENT TRIMOLECULAR COMPLEX OF C1Q, R
CC AND S IN THE MOLAR RATION OF 1:2:2. THE C1Q SUBCOMPONENT IS
CC COMPOSED OF NINE SUBUNITS, SIX OF WHICH ARE DISULFIDE-LINKED
CC DIMERS OF THE A AND B CHAINS, AND THREE OF WHICH ARE DISULFIDE-
CC LINKED DIMERS OF THE C CHAIN. IN ADDITION TO THE MAJOR A:B AND C:C
CC LINKED BANDS, RAT, UNLIKE HUMAN C1Q, CONTAINED MINOR DIMER SPECIES.
CC -!- SIMILARITY: Contains 1 collagenous domain.
DR InterPro: IPR001073; C1q.
DR PROSITE: PS01113; C1Q; PARTIAL.
KW Complement pathway; Plasma; Hydroxylation; Glycoprotein; Collagen;
KW Repeat.
FT DISULFID 4 4 INTERCHAIN (WITH C-4 IN B CHAIN).
FT NON_TER 15 15
SQ SEQUENCE 15 AA; 1488 MW; 1B3D3000B7793965 CRC64;

Query Match 23.9%; Score 21; DB 1; Length 15;
Best Local Similarity 44.4%; Pred. No. 1.5e+03;
Matches 4; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

CY 2 RYPSGNCGL 10
DB 5 RAPNGKQGV 13

RESULT 12
FGF1_CANFA STANDARD; PRT; 15 AA.
ID FGF1_CANFA
AC P18651;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Heparin-binding growth factor 1 (HBGF-1) (Acidic fibroblast growth
DE factor) (AFGF) (Alpha-endothelial cell growth factor) (Fragment).
GN FGF1 OR FGF-1.
CS Canis familiaris (Dog).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
OX NCBI_TaxID=9615;
RN [1]
PP SEQUENCE.
RX MEDLINE=89231704; PubMed=2714282;
Quinkler W., Maasberg M., Bernotat-Danielowski S., Luethke N.,
RA Sharma H.S., Schaper W.;
RT "Isolation of heparin-binding growth factors from bovine, porcine and
RT canine hearts.";
RL Eur. J. Biochem. 181:67-73(1989).
CC -!- FUNCTION: THE HEPARIN-BINDING GROWTH FACTORS ARE ANGIOGENIC AGENTS
CC IN VIVO AND ARE POTENT MITOGENS FOR A VARIETY OF CELL TYPES IN
CC VITRO. THERE ARE DIFFERENCES IN THE TISSUE DISTRIBUTION AND
CC CONCENTRATION OF THESE 2 GROWTH FACTORS.
CC -!- SUBUNIT: Monomer.
CC -!- MISCELLANEOUS: THIS PROTEIN BINDS HEPARIN, ALTHOUGH LESS STRONGLY
CC THAN DOES BFGF.
CC -!- SIMILARITY: BELONGS TO THE HEPARIN-BINDING GROWTH FACTORS FAMILY.
DR PIR: S01955; S01955.
DR InterPro: IPR002348; IL1_HBGF.
DR PROSITE: PS00247; HBGF_FGF; PARTIAL.
KW Growth factor; Mitogen; Angiogenesis; Heparin-binding.
FT NON_TER 15 15
SQ SEQUENCE 15 AA; 1732 MW; 53CC9A3CADDDEAA1 CRC64;

Query Match 23.9%; Score 21; DB 1; Length 15;
Best Local Similarity 66.7%; Pred. No. 1.5e+03;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

CY 1C LYSSG 15
DB 8 LYXSG 13

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Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

```

RESULT 13
PPCK_FASHE STANDARD; PRT; 10 AA.
AC P80525;
DT 01-FEB-1995 (Rel. 33, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE Putative phosphoenolpyruvate carboxykinase (GTP) [EC 4.1.1.22;
DE (phosphoenolpyruvate carboxylase) (PECK) (Newly excysted juvenile
DE protein 1) (fragment)].
OS Fasciola hepatica (Liver fluke).
OC Eukaryota; Metazoa; Platyhelminthes; Trematoda; Digenea;
OC Echinostomida; Echinostomata; Fascioloidae; Fasciolidae; Fasciola.
OX NCBI_TaxID=6192;
RN [1]
RP SEQUENCE.
RX MEDLINE=95366993; PubMed=7639732;
RA Tkalcovic J., Ashman K., Meesjen E.;
RT "Fasciola hepatica: rapid identification of newly excysted juvenile
RT proteins."
RL Biochem. Biophys. Res. Commun. 213:169-174 (1995).
CC -1- CATALYTIC ACTIVITY: GTP + oxaloacetate = GDP + phosphoenolpyruvate
CC + CO(2);.
CC -1- SIMILARITY: BELONGS TO THE PHOSPHOENOLPYRUVATE CARBOXYKINASE (GTP)
CC FAMILY.
DR InterPro; IPR000364; PEP carboxykin.
DR PROSITE; PS00505; PEPCK.GTP; PARTIAL.
KW Lyase; Decarboxylase; GTP-binding.
FT NON_TER 10
SQ SEQUENCE 10 AA; 169 MW; 8393AG187AA9C87A CRC64;

```

Query Match 22.7%; Score 20; DB 1; Length 10;
 Best Local Similarity 75.0%; Pred. No. 1.4e+03;
 Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```

QY 3 YPSG 6
DB 1 YPDG 4

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```

RESULT 14
TKL1_LOCMI STANDARD; PRT; 9 AA.
AC P-6223;
DT 01-APR-1990 (Rel. 14, Created)
DT 01-APR-1990 (Rel. 14, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Locustatachykinin I (TK-I).
OS Locusta migratoria (Migratory locust).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Orthopteroidea; Orthoptera; Caelifera; Acridoidea;
OC Acridoidea; Acrididae; Oedipodinae; Locusta.
OX NCBI_TaxID=7024;
RN [1]
RP SEQUENCE.
RX MEDLINE=90184489; PubMed=2311766;
RA Schoofs L., Holman G.M., Hayes T.K., Nachman R.J., de Loof A.;
RT "Locustatachykinin I and II, two novel insect neuropeptides with
RT homology to peptides of the vertebrate tachykinin family."
RL FEBS Lett. 261:397-401 (1990).
CC -1- FUNCTION: MYOACTIVE PEPTIDE. STIMULATES THE CONTRACTION OF THE
CC OVIDUCT AND FOREGUT.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- SIMILARITY: SOME SIMILARITY TO TACHYKININS.
KW Tachykinin; Neuropeptide; Amidation.
FT MOD_RES 9
FT SEQUENCE 9 AA; 939 MW; 2389C86B59C865A7 CRC64;

```

Query Match 21.6%; Score 19; DB 1; Length 9;
 Best Local Similarity 57.1%; Pred. No. 1.3e+05;

```

QY 4 PSQKGL 10
DB 2 PSQFQGV 8

RESULT 15
HTF_HEUZE STANDARD; PRT; 10 AA.
AC P-6153;
DT 01-AUG-1990 (Rel. 15, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Hypertrehalosaemic hormone (HeZ-HRTH).
OS Heliothis zea (Corn earworm) (Bollworm).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia; Noctuoidea;
OC Noctuidae; Heliothinae; Helicoverpa.
OX NCBI_TaxID=7113;
RN [1]
RP SEQUENCE.
RX MEDLINE=88326324; PubMed=3415690;
RA Gaffe H., Reina A.K., Riley C.T., Fraser B.A., Bird T.G.,
RA Tseng C.M., Zhang Y.S., Hayes D.K.;
RT "Isolation and primary structure of a neuropeptide hormone from
RT Heliothis zea with hypertrehalosemic and adipokinetic activities."
RL Biochem. Biophys. Res. Commun. 155:344-350 (1988).
CC -1- FUNCTION: HYPERTREHALOSAEMIC FACTORS ARE NEUROPEPTIDES THAT
CC ELEVATE THE LEVEL OF TREHALOSE IN THE HEMOLYMPH OF INSECTS).
CC THE MAJOR CARBOHYDRATE IN THE HEMOLYMPH OF INSECTS).
CC -1- SIMILARITY: BELONGS TO THE AKH / HRTH / RPCH FAMILY.
DR P-R; A3:571; A31571.
DR InterPro; IPR002047; AKH.
DR PROSITE; PS00256; AKH; 1.
KW Neuropeptide; Amidation; Pyroglutamate carboxylic acid.
FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
FT SEQUENCE 10 AA; 1096 MW; 8E70367865A5B9D1 CRC64;

```

Query Match 21.6%; Score 19; DB 1; Length 10;
 Best Local Similarity 66.7%; Pred. No. 2.1e+03;
 Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

```

QY 1C LYSSG 15
DB 2 LTFSSG 7

```

Search completed: November 5, 2003, 16:57:50
 Job time : 13 secs

GenCore version 5.1.6
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Query protein - protein search, using sw mode:

Run on: November 5, 2003, 16:54:56 ; Search time 33 seconds
(without alignments)
117.297 Million cell updates/sec

Title: US-09-902-563-18

Perfect score: 88

Sequence: 1 DRYPSGNGLYYSSG 15

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 830525 seqs, 256052604 residues

Total number of hits satisfying chosen parameters: 3526

Minimum DB seq length: 0

Maximum DB seq length: 15

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL23:

- 1: sp archaea:
- 2: sp bacteria:
- 3: sp fungi:
- 4: sp human:
- 5: sp invertebrate:
- 6: sp mammal:
- 7: sp mhc:
- 8: sp organelle:
- 9: sp phage:
- 10: sp plant:
- 11: sp rodent:
- 12: sp virus:
- 13: sp vertebrate:
- 14: sp unclassified:
- 15: sp virus:
- 16: sp bacterioph:
- 17: sp archaea:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	DB ID	Description
1	27	30.7	10 P82436	P82436 nicotiana t
2	25	28.4	13 5 Q8T6E9	Q8T6E9 nicotiana t
3	25	28.4	13 5 Q8T6E9	Q8T6E9 nicotiana t
4	24	27.3	9 4 Q96T78	Q96T78 homo sapien
5	24	27.3	11 2 Q9A1Y6	Q9A1Y6 carsonella
6	24	27.3	11 5 Q9N165	Q9N165 ascaris su
7	23	26.1	14 13 Q9J80	Q9J80 streptococci
8	22	25.0	10 6 Q9WPC4	Q9WPC4 ateles belz
9	22	25.0	11 13 Q9CWA2	Q9CWA2 gallus gall
10	22	25.0	15 4 C03604	C03604 homo sapien
11	22	25.0	15 8 Q95770	Q95770 cyclura ric
12	22	25.0	15 13 Q9PR29	Q9PR29 micropogoni
13	21	23.9	10 13 Q9CY93	Q9CY93 gallus gall
14	21	23.9	13 4 Q9UPE7	Q9UPE7 homo sapien
15	21	23.9	13 11 Q8CJ33	Q8CJ33 mus musculu
16	21	23.9	15 10 Q9S8V7	Q9S8V7 tritium ae

17	20	22.7	10 4 Q8NEY3	Q8NEY3 homo sapien
18	20	22.7	12 2 Q930U4	Q930U4 escherichia
19	20	22.7	12 4 Q9UMQ9	Q9UMQ9 homo sapien
20	20	22.7	13 11 Q9WT26	Q9WT26 mus musculu
21	20	22.7	13 11 P82808	P82808 rattus norv
22	20	22.7	14 2 Q45876	Q45876 elostridium
23	20	22.7	14 2 Q45872	Q45872 elostridium
24	20	22.7	14 12 Q9PY99	Q9PY99 murine hepa
25	20	22.7	15 4 Q9JU51	Q9JU51 homo sapien
26	20	22.7	15 12 Q86869	Q86869 lymphocytic
27	20	22.7	15 12 Q86865	Q86865 lymphocytic
28	20	22.7	15 12 Q86867	Q86867 lymphocytic
29	19	21.6	7 1C Q9C5B3	Q9C5B3 arabidopsis
30	19	21.6	8 7 Q9S213	Q9S213 arctolagus
31	19	21.6	10 4 Q15342	Q15342 homo sapien
32	19	21.6	13 4 Q9UCRC	Q9UCRC homo sapien
33	19	21.6	13 4 Q9UC27	Q9UC27 homo sapien
34	19	21.6	15 1 Q9UWH6	Q9UWH6 thermococu
35	19	21.6	15 10 Q9S8L4	Q9S8L4 zea mays (m
36	18	20.5	3 6 Q9TRU7	Q9TRU7 bos taurus
37	18	20.5	9 11 Q9QWT0	Q9QWT0 mus musculu
38	18	20.5	9 11 C08979	C08979 mus musculu
39	18	20.5	1C 2 Q9X533	Q9X533 escherichia
40	18	20.5	1C 2 Q9X534	Q9X534 leclercia a
41	18	20.5	1C 2 Q48469	Q48469 klebsiella
42	18	20.5	11 5 Q9TWN2	Q9TWN2 aplysia cal
43	18	20.5	11 12 Q86866	Q86866 lymphocytic
44	18	20.5	11 12 Q86864	Q86864 lymphocytic
45	18	20.5	11 12 Q86868	Q86868 lymphocytic

ALIGNMENTS

RESULT 1

P82436
IC P82436 PRELIMINARY; PRT; 10 AA.
AC P82436
DT 01-JUN-2000 (TrEMBLrel. 14, Created)
ET 01-JUN-2000 (TrEMBLrel. 14, Last sequence update)
DT 01-JUN-2000 (TrEMBLrel. 14, Last annotation update)
DE 50 kDa cell wall protein (Fragment).
OS Nicotiana tabacum (Common tobacco).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
CC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
CC Asteridae; Lamiales; Solanales; Solanaceae; Nicotiana.
OX NCBI_TaxID=4097;
RN 11
RP SEQUENCE.
RC STRAIN=cv. PETIT HAVANA;
RA Blee K.A., Bonham V.A., Mitchell G.P., Robertson D., Slabas A.R.,
RA Wojtaszek P., Bolwell G.P.;
RT "Proteomic study of secondary cell wall proteins from transformed
RT tobacco culture";
RL Planta 0:0-0(2000).
CC -!- SUBCELLULAR LOCATION: CELL WALL.
CC -!- TISSUE SPECIFICITY: XYLEM.
KW Cell wall.
FT NON-TER 10 10
SQ SEQUENCE 10 AA; 1126 MW; C68E32486AF77B46 CRC64;

Query Match 32.7%; Score 27; DB 10; Length 10;

Best Local Similarity 66.7%; Pred. No. 5.9e+02;

Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

CY 2 RYPSGN 7

DB 3 QYPXGN 8

RESULT 2

Q8T6E9
ID Q8T6E9 PRELIMINARY; PRT; 13 AA.

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AC Q8T659;
DC 01-JUN-2002 (TXEMBLrel. 2); Created;
DT 01-JUN-2002 (TXEMBLrel. 2); Last sequence update;
DT 01-OCT-2002 (TXEMBLrel. 2); Last annotation update;
DE Myocyte enhancing factor 2 (Fragment).
GN MEF2.
CS Drosophila miranda (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7229;
RN [1]
RP SEQUENCE FROM N.A.
RA Schaeffer S.W., Goetting-Minesky M.P., Kovacevic M., Peoples J.,
RA Graybill J.L., Miller C.M., Kim K., Nelson J.G., Anderson W.W.;
RT "Evolutionary genomics of inversions in Drosophila pseudoobscura:
RT Modes of selection.";
RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF476747; AAL91745.1;
DR EMBL; AF476748; AAL91746.1;
DR EMBL; AF476749; AAL91747.1;
DR EMBL; AF476750; AAL91748.1;
DR EMBL; AF476751; AAL91749.1;
DR EMBL; AF476752; AAL91750.1;
DR EMBL; AF476753; AAL91751.1;
DR EMBL; AF476754; AAL91752.1;
DR EMBL; AF476755; AAL91753.1;
DR EMBL; AF476756; AAL91754.1;
DR EMBL; AF476757; AAL91755.1;
DR EMBL; AF476758; AAL91756.1;
DR EMBL; AF476759; AAL91757.1;
DR EMBL; AF476760; AAL91758.1;
DR EMBL; AF476761; AAL91759.1;
DR EMBL; AF476762; AAL91760.1;
DR EMBL; AF476763; AAL91761.1;
DR EMBL; AF476764; AAL91762.1;
DR EMBL; AF476765; AAL91763.1;
DR EMBL; AF476766; AAL91764.1;
DR EMBL; AF476767; AAL91765.1;
DR EMBL; AF476768; AAL91766.1;
DR EMBL; AF476769; AAL91767.1;
DR EMBL; AF476770; AAL91768.1;
DR EMBL; AF476771; AAL91769.1;
DR EMBL; AF476772; AAL91770.1;
DR EMBL; AF476773; AAL91771.1;
DR EMBL; AF476774; AAL91772.1;
DR EMBL; AF476775; AAL91773.1;
DR EMBL; AF476776; AAL91774.1;
DR EMBL; AF476777; AAL91775.1;
DR EMBL; AF476778; AAL91776.1;
DR EMBL; AF476779; AAL91777.1;
DR EMBL; AF476780; AAL91778.1;
DR EMBL; AF476781; AAL91779.1;
DR EMBL; AF476782; AAL91780.1;
DR EMBL; AF476783; AAL91781.1;
DR EMBL; AF476784; AAL91782.1;
DR EMBL; AF476785; AAL91783.1;
DR EMBL; AF476786; AAL91784.1;
DR EMBL; AF476787; AAL91785.1;
DR EMBL; AF476788; AAL91786.1;
DR EMBL; AF476789; AAL91787.1;
DR EMBL; AF476790; AAL91788.1;
DR EMBL; AF476791; AAL91789.1;
DR EMBL; AF476792; AAL91790.1;
DR EMBL; AF476793; AAL91791.1;
DR EMBL; AF476794; AAL91792.1;
DR EMBL; AF476795; AAL91793.1;
DR EMBL; AF476796; AAL91794.1;
DR EMBL; AF476797; AAL91795.1;
DR EMBL; AF476798; AAL91796.1;
DR EMBL; AF476799; AAL91797.1;
DR EMBL; AF476800; AAL91798.1;
DR EMBL; AF476801; AAL91799.1;
DR EMBL; AF476802; AAL91800.1;
DR EMBL; AF476803; AAL91801.1;
DR EMBL; AF476804; AAL91802.1;
DR EMBL; AF476805; AAL91803.1;
DR EMBL; AF476806; AAL91804.1;
DR EMBL; AF476807; AAL91805.1;
DR EMBL; AF476808; AAL91806.1;
DR EMBL; AF476809; AAL91807.1;
DR EMBL; AF476810; AAL91808.1;
DR EMBL; AF476811; AAL91809.1;
DR EMBL; AF476812; AAL91810.1;
DR EMBL; AF476813; AAL91811.1;
DR EMBL; AF476814; AAL91812.1;
DR EMBL; AF476815; AAL91813.1;
DR EMBL; AF476816; AAL91814.1;
DR EMBL; AF476817; AAL91815.1;
DR FlyBase; FBgn0062239; Dmir\Wef2.
FT NON_TER 13
FT NON_TER 13
SQ SEQUENCE 13 AA; 158F380B6BE05050 CRC64;
Query Match 28.4%; Score 25; DB 5; Length 13;
Best Local Similarity 80.0%; Pred. No. 1.7e+03;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 3 YPSGN 7
Db 8 YPSGS 12
RESULT 3
Q8STIS PRELIMINARY; PRT; 13 AA.
AC Q8STIS;
DT 01-JUN-2002 (TXEMBLrel. 2); Created;
DT 01-JUN-2002 (TXEMBLrel. 2); Last sequence update;
DT 01-OCT-2002 (TXEMBLrel. 2); Last annotation update;
DE Myocyte enhancing factor 2 (Fragment).
GN MEF2.
CS Drosophila pseudoobscura (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7237;
RN [1]
RP SEQUENCE FROM N.A.
RA Schaeffer S.W., Goetting-Minesky M.P., Kovacevic M., Peoples J.,
RA Graybill J.L., Miller C.M., Kim K., Nelson J.G., Anderson W.W.;
RT "Evolutionary genomics of inversions in Drosophila pseudoobscura:
RT Modes of selection.";
RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF476728; AAL91726.1;
DR EMBL; AF476729; AAL91727.1;
DR EMBL; AF476730; AAL91728.1;
DR EMBL; AF476731; AAL91729.1;
DR EMBL; AF476732; AAL91730.1;
DR EMBL; AF476733; AAL91731.1;
DR EMBL; AF476734; AAL91732.1;
DR EMBL; AF476735; AAL91733.1;
DR EMBL; AF476736; AAL91734.1;
DR EMBL; AF476737; AAL91735.1;
DR EMBL; AF476738; AAL91736.1;
DR EMBL; AF476739; AAL91737.1;
DR EMBL; AF476740; AAL91738.1;
DR EMBL; AF476741; AAL91739.1;
DR EMBL; AF476742; AAL91740.1;
DR EMBL; AF476743; AAL91741.1;
DR EMBL; AF476744; AAL91742.1;
DR EMBL; AF476745; AAL91743.1;
DR EMBL; AF476746; AAL91744.1;

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SQ SEQUENCE 13 AA; 1313 MW; 15BF380B6BE05050 CRC64;

Query Match 28.4%; Score 25; DB 5; Length 13;
Best Local Similarity 80.0%; Pred. No. 1.7e+03;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 YPSGN 7
DB 8 YPSGS 12

RESULT 4

Q96T78 PRELIMINARY; PRT; 9 AA.

AC Q96T78; 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE Contactin-associated protein 2 (Fragment).
GN CNTNAP2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Placentalia; Catarrhini; Hominoidea; Homo.
OX NCBI_TaxID=9606;
RN [1];
RP SEQUENCE FROM N.A.
RX MEDLINE=21250995; PubMed=11359571;
RA Nakabayashi K., Scherer S.W.;
RT "The human contactin-associated protein 2 (CNTNAP2) spans over 2 Mb of
DNA at chromosome 7q35.";
RL Genomics 73:108-112(2001).
DR EMBL; AF182295; AAK49906.1; -.
FT NON_TER 1
FT NON_TER 9
SQ SEQUENCE 9 AA; 1080 MW; 9139A2D5A7B51EA CRC64;

Query Match 27.3%; Score 24; DB 4; Length 9;
Best Local Similarity 80.0%; Pred. No. 8.3e+05;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 DRYPS 5
DB 2 DRYPS 6

RESULT 5

Q9A1Y6 PRELIMINARY; PRT; 11 AA.

AC Q9A1Y6; 01-JUN-2001 (TREMBLrel. 17, Created)
DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE Trypoptanylin-1 RNA synthetase (Fragment).
GN TRPS.
OS Carsonella ruddii.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Candidatus Carsonella.
OX NCBI_TaxID=14196;
RN [1];
RP SEQUENCE FROM N.A.
RX MEDLINE=20336438; PubMed=10877784;
RA Thao M.L., Moran N.A., Abbot P., Brennan E.B., Burckhardt D.H.,
BAumann P.;
RT "Cooperation of psyllids and their primary prokaryotic
endosymbionts.";
RL Appl. Environ. Microbiol. 66:2898-2905(2000).
RN [2];
RP SEQUENCE FROM N.A.
RX MEDLINE=21225546; PubMed=11222582;
RA Clark M.A., Baumann L., Thao M.L., Moran N.A., Baumann P.;
RT "Degenerative Minimalism in the Genome of a Psyllid Endosymbiont.";
RL J. Bacteriol. 183:1853-1861(2001).
DR EMBL; AF211138; AAK15388.1; -.
KW Aminoacyl-tRNA synthetase.

FT NON_TER 1
SQ SEQUENCE 11 AA; 1295 MW; 0CA993A5345B5720 CRC64;

Query Match 27.3%; Score 24; DB 2; Length 11;
Best Local Similarity 42.9%; Pred. No. 2e+03;
Matches 3; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 7 NCGLYYS 13
DB 1 NCGLYN 7

RESULT 6

Q9NL65 PRELIMINARY; PRT; 11 AA.

AC Q9NL65; 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DT 01-OCT-2000 (TREMBLrel. 15, Last annotation update)
DE ASABF-delta (Fragment).
GN ASABF-DELTA.
OS Ascaris suum (Pig roundworm) (Ascaris lumbricoides).
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Ascaridida; Ascaridoidea;
OC Ascarididae; Ascaris.
OX NCBI_TaxID=6253;
RN [1];
RP SEQUENCE FROM N.A.
RA Kato Y.;
RT "Ascaris suum asabf-delta gene, exon 2.";
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB029815; BAA89496.1; -.
FT NON_TER 1
FT NON_TER 11
SQ SEQUENCE 11 AA; 1187 MW; 8EADDD3CD:EAB5861 CRC64;

Query Match 27.3%; Score 24; DB 5; Length 11;
Best Local Similarity 56.7%; Pred. No. 2e+03;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 7 NCGLYY 12
DB 1 NCGLGY 6

RESULT 7

Q8JC80 PRELIMINARY; PRT; 14 AA.

AC Q8JC80; 01-OCT-2002 (TREMBLrel. 22, Created)
DT 01-OCT-2002 (TREMBLrel. 22, Last sequence update)
DT 01-OCT-2002 (TREMBLrel. 22, Last annotation update)
DE Beta fibrinogen (Fragment).
OS Streptopelia bitorquata.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Columbiformes; Columbidae;
OC Streptopelia.
OX NCBI_TaxID=177146;
RN [1];
RP SEQUENCE FROM N.A.
RA Johnson K.P., de Kort S., Dinwoodey K., Mateman A.C., ten Cate C.,
PA Lessells C.V., Clayton D.H.;
RT "A molecular phylogeny of the dove genera Streptopelia and Columba.";
RJ Auk 118:874-887(2001).
DR EMBL; AF353457; AAM22349.1; -.
DR InterPro; IPR002181; Fibrinogen_C.
DR Pfam; PF00147; fibrinogen_C; 1.
FT NON_TER 1
FT NON_TER 14
SQ SEQUENCE 14 AA; 1655 MW; 9AF33468DAC04D41 CRC64;

Query Match 26.1%; Score 23; DB 13; Length 14;
Best Local Similarity 50.0%; Pred. No. 3.8e+03;
Matches 3; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 9 GLYSS 14
|:|:|
Db 2 GMYST 7

RESULT 8

Q9WFO4 PRELIMINARY; PRT; 10 AA.
AC Q9WFO4
CT 01-MAR-2002 (TREMBlrel. 20, Created)
DT 01-MAR-2002 (TREMBlrel. 20, Last sequence update)
DE 01-MAR-2002 (TREMBlrel. 20, Last annotation update)
GN Oculocutaneous albinism type II (Fragment)
OS Ateles belzebuth chamek (Chamek spider monkey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Platyrrhini; Cebidae; Ateles.
OX NCBI_TaxID=118643;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21636947; PubMed=11778586;
RA Seanez H.N., Lima C.R., Lemos B., Borvicino C.R., Moreira M.A.X.,
Canavez F.C.
RT "Gene assignment in Ateles paniscus chamek (Platyrrhini, Primates).
Allocation of 19 markers of human syntenic groups 1,2,7,14,15,17 and
22.";
RL Chromosome Res. 9:631-639(2001).
DR EMBL: AF375652; M231489.1;
FT NON TER 1
SQ SEQUENCE 10 AA; 901 MW; 22DF477DD87EA5B6 CRC64;

Query Match 25.0%; Score 22; DB 6; Length 10;
Best Local Similarity 75.0%; Pred. No. 4e+03;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 6 GNCG 9
|:|:|
Db 3 GSCG 6

RESULT 9

Q9QWA2 PRELIMINARY; PRT; 11 AA.
AC Q9QWA2
CT 01-DEC-2001 (TREMBlrel. 19, Created)
DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
DE Extracellular fatty acid binding protein (Fragment).
GN Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OX Gallus.
OX NCBI_TaxID=9031;
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Blood;
RA Wang Q., Li N., Deng X., Li H.;
RT "Single Nucleotide Polymorphism Analysis on Encoding Region of
Extracellular Fatty Acid Binding Protein Genes and Their Associations
With the Fattiness Trait in Chicken."
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF402001; AAK94062.1;
FT NON TER 1
FT NON TER 11
SQ SEQUENCE 11 AA; 1277 MW; 873417F02B187AAA CRC64;

Query Match 25.0%; Score 22; DB 13; Length 11;
Best Local Similarity 100.0%; Pred. No. 4.4e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 LYYS 13
|:|:|

Db 9 DYYS 11

RESULT 10

Q0C604 PRELIMINARY; PRT; 15 AA.
AC Q0C604
CT 01-JUL-1997 (TREMBlrel. 04, Created)
DT 01-JUL-1997 (TREMBlrel. 04, Last sequence update)
DE 01-MAR-2001 (TREMBlrel. 16, Last annotation update)
DB Type I collagen alpha 1(I) chain (Fragment).
GN COL1A1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=96336021; PubMed=9757037;
RA Mayer S.A., Rubin B.S., Starman B.J., Byers P.H.;
RT "Spontaneous multivessel cervical artery dissection in a patient with
a substitution of alanine for glycine (G13A) in the alpha 1(I) chain
of type I collagen."
RL Neurology 47:552-556(1996).
DR EMBL: S83355; AAB50780.2;
KW Collagen.
FT NON TER 1
FT NON TER 15
SQ SEQUENCE 15 AA; 1413 MW; 4CA8D720AAF780FC CRC64;

Query Match 25.0%; Score 22; DB 4; Length 15;
Best Local Similarity 71.4%; Pred. No. 6e+03;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4 PSGNCG 10
|:|:|
Db 2 PSGPRGL 8

RESULT 11

Q95770 PRELIMINARY; PRT; 15 AA.
AC Q95770
CT 01-FEB-1997 (TREMBlrel. 02, Created)
DT 01-FEB-1997 (TREMBlrel. 02, Last sequence update)
DE 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
GN NADH dehydrogenase subunit 4 (Fragment).
OX ND4.
OC Cyclura ticordi.
OC Mitochondrion.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Iguania; Iguanidae; Iguaninae; Cyclura.
OX NCBI_TaxID=51215;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97019047; PubMed=8865663;
RA Sites J.W. Jr., Davis S.K., Guerra T., Iverson J.B., Snell H.L.;
RT "Character congruence and phylogenetic signal in molecular and
morphological data sets: a case study in the living Iguanas (Squamata,
Iguanidae)."
RL Mol. Biol. Evol. 13:1087-1105(1996).
DR EMBL: U66237; AAB07473.1;
KW Mitochondrion.
FT NON TER 1
FT NON TER 15
SQ SEQUENCE 15 AA; 1715 MW; 8327178E7927A57E CRC64;

Query Match 25.0%; Score 22; DB 8; Length 15;
Best Local Similarity 50.0%; Pred. No. 6e+03;
Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 7 NCGLYSS 14
|:|:|
Db 2 NCLRLST-S 9


```

RESULT 12
Q9PRZ9
ID Q9PRZ9 PRELIMINARY; PRT; 15 AA.
AC Q9PRZ9
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
DE Gonadotropin I beta subunit (Fragment).
CS Microgogonias undulatus (Atlantic Croaker).
CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
CC Actinopterygii; Neopterygii; Teleostei; Euteleostomi; Neoteleostomi;
CC Acanthomorpha; Acanthopterygii; Percormorpha; Perciformes; Percidae;
CC Sclaeidae; Microgogonias.
CX NCBI_TaxID=29154;
RN [1]
RP SEQUENCE.
RX MEDLINE=94010173; PubMed=8405893;
RA Copeiland P.A., Thomas P.;
RT "Isolation of gonadotropin subunits and evidence for two distinct
gonadotropins in Atlantic croaker (Microgogonias undulatus).";
RJ Gen. Comp. Endocrinol. 91:115-125(1993).
SQ SEQUENCE 15 AA; 1732 MW; 81709992C3D86A4A CRC64;

Query Match 25.0%; Score 22; DB 13; Length 15;
Best Local Similarity 75.0%; Pred. No. 6e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 CSGLY 11
DB 4 CGFY 7

RESULT 13
Q90Y93
ID Q90Y93 PRELIMINARY; PRT; 10 AA.
AC Q90Y93
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Growth hormone (Fragment).
CS Gallus.
CX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RA Katsaki N., Nakada A., Yagi E., Okabayashi H., Guemene D.;
RT "Genetic variation of chicken growth hormone gene.";
RL Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB061722; BAB69037.1; -.
FT NON-TER 1
FT NON-TER 10
SQ SEQUENCE 10 AA; 1155 MW; 6841751775A40AAB CRC64;

Query Match 23.9%; Score 21; DB 13; Length 10;
Best Local Similarity 66.7%; Pred. No. 5.8e+03;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 DRYPFG 6
DB 4 DRSPRG 9

RESULT 14
Q9UPE7
ID Q9UPE7 PRELIMINARY; PRT; 13 AA.
AC Q9UPE7
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)

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DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Inosine monophosphatase 2 (Fragment).
GN IMPA2.
OS Homo sapiens (Human).
CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
CC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
CX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97463449; PubMed=9322233;
RA Yoshikawa T., Turner G., Esterling L.E., Sanders A.R.,
RA Decera-Wadleigh S.D.;
RT "A novel human myo-inositol monophosphatase gene, IMP18p, maps to a
susceptibility region for bipolar disorder.";
RJ Mol. Psychiatry 2:393-397(1997).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=20284187;
RA Yoshikawa T., Padigaru M., Karkera J.D., Sharma M., Berrettini W.H.,
RA Esterling L.E., Detera-Wadleigh S.D.;
RT "Genomic structure and novel variants of myo-inositol monophosphatase
2.";
RJ Mol. Psychiatry 5:165-171(2000).
DR EMBL; AF025882; AAD22136.1; -.
DR EMBL; AF025881; AAD22136.1; JOINED.
FT NON-TER 1
FT NON-TER 13
SQ SEQUENCE 13 AA; 1589 MW; F3415D841F48D401 CRC64;

Query Match 23.9%; Score 21; DB 4; Length 13;
Best Local Similarity 60.0%; Pred. No. 7.6e+03;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 DRYPFS 5
DB 1 ERPS 5

RESULT 15
Q8CJ33
ID Q8CJ33 PRELIMINARY; PRT; 13 AA.
AC Q8CJ33
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Myoneurin (Fragment).
CS Mus musculus (Mouse).
CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
CX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=BALB/c; TISSUE=Kidney;
RC MEDLINE=20334280; PubMed=10873615;
RA Alliel P.M., Seddiqi N., Goudou D., Cifuentes-Diaz C., Romero N.,
RA Velasco E., Rieger P., Perin J.P.;
RT "Myoneurin, a novel member of the BTB/POZ-zinc finger family highly
expressed in human muscle.";
RJ Biochem. Biophys. Res. Commun. 273:385-391(2000).
RN [2]
RP SEQUENCE FROM N.A.
RX STRAIN=BALB/c; TISSUE=Kidney;
RA Bitoun M., Perin J.P., Seddiqi N., Goudou D., Camuzat A., Matter M.G.,
RA Rieger P., Alliel P.M.;
RT "The human and mouse myoneurin genes: Genomic organization, splice
variants, chromosomal mapping and flanking genes.";
RJ Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF530454; AAN28707.1; -.
FT NON-TER 1
FT NON-TER 13
SQ SEQUENCE 13 AA; 1445 MW; 9CB68B708CA1587E CRC64;

Query Match 23.9%; Score 21; DB 11; Length 13;

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Best Local Similarity 57.1%; Pred. No. 7.6e+03;
Matches 4; Conservative 0; Mismatches 3; Index 0; Gaps 0;
Oy 3 YPSGCG 9
| | |
Db 4 YICGCG 10

Search completed: November 5, 2003, 16:58:37
Job time : 36 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 5, 2003, 16:43:21 : Search time 41 seconds
(without alignment)
59.071 Million cell updates/sec

Title: US-09-902-563-18

Perfect score: 88

Sequence: 1 DRYPSGNGLYSSG 15

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1107863 seqs, 158726573 residues

Total number of hits satisfying chosen parameters: 350435

Minimum DB seq length: 6

Maximum DB seq length: 15

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

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- 24: /SIDSI/gcgdata/genseq/genseqp-emb/AA2003.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	88	100.0	15	AAW88237	Human prothrombina
2	37	42.0	14	AAE28619	Human X-betaV2 pro
3	33	37.5	9	AAU23853	Human MHC Class I
4	33	37.5	9	AAU24319	Human MHC Class I
5	33	37.5	9	AAU24423	Human MHC molecule
6	33	37.5	9	AAU24441	Human MHC molecule
7	33	37.5	10	AAU24484	Human MHC molecule
8	33	37.5	12	AAAB2604	Human IgE C-epsilo
9	33	37.5	12	AAU16769	Peptide EED16/47/4

10	33	37.5	12	23	ABJ00390	Human IgE cyclic i
11	33	37.5	15	18	AAW23509	Purified cis-9,10-
12	33	37.5	15	19	AAWS7788	Fatty acid amide h
13	31	35.2	10	22	AAAG96214	Human complementar
14	31	35.2	15	5	AAAP40328	Sequence of concto
15	31	35.2	15	16	AAAT75265	Alpha-corotoxin GI
16	31	35.2	15	18	AAAT75265	Alpha-corotoxin GI
17	30.5	34.7	15	24	ABR34060	Human cancer-relat
18	30.5	34.7	15	24	ABR34060	Human cancer-relat
19	30	34.1	7	20	AAV30230	Physarum polyceph
20	30	34.1	10	22	AAV30230	Physarum polyceph
21	30	34.1	12	20	AAV29882	Human comp-ementar
22	30	34.1	13	15	AAV29882	Human comp-ementar
23	30	34.1	14	15	AAV29882	Human comp-ementar
24	30	34.1	14	19	AAV59655	PH 2.5 acid phosph
25	30	34.1	14	22	AAV59655	Hypotensive polype
26	30	34.1	14	22	AAV59655	Amino acid sequenc
27	30	34.1	14	22	AAV59655	Peptide derived fr
28	30	34.1	14	22	AAV59655	Peptide derived fr
29	30	34.1	14	22	AAV59655	Peptide derived fr
30	30	34.1	15	16	AAV59655	Cryoglobulinemia t
31	30	34.1	15	19	AAV59655	Human P512 proteol
32	30	34.1	15	23	AAV59655	Physarum polyceph
33	30	34.1	15	21	AAV59655	Antigen peptide de
34	30	34.1	15	22	AAV59655	Human actin 14 pep
35	29	33.0	10	22	AAU24373	Human MHC class I
36	29	33.0	10	22	AAU24373	Human MHC class I
37	29	33.0	14	14	AAE69323	Human VHC molecule
38	29	33.0	14	21	AAE69323	Gp 11b/IIa recept
39	29	33.0	14	21	AAE69323	Human ERV2 protein
40	29	33.0	15	20	AAV07427	Fibrin polymerizat
41	29	33.0	15	20	AAV07427	HSV-1 TK amino aci
42	29	33.0	15	20	AAV07427	HSV-1 TK amino aci
43	28	31.8	6	24	ABF56238	Transforming growt
44	28	31.8	7	23	AAU11469	Thymidine kinase (
45	28	31.8	8	19	AAW63298	Targeting moiety p

ALIGNMENTS

RESULT 1
AAW88237
ID AAW88237 standard; Peptide; 15 AA.
XX
AC AAW88237;
XX
DT 15-MAR-1999 (first entry)
XX
DE Human prothrombinase Fgl2 epitope.
XX
KW Prothrombinase; hfgi2; Fgl2; human; immune coagulation; antibody;
KW inhibitor; infection; graft rejection; glomerulonephritis; cancer;
KW gastrointestinal disease; foetal loss; therapy; vaccine; epitope.
XX
CS Homo sapiens.
XX
FN WO9851335-A1.
XX
PD 19-NOV-1998.
XX
PF 15-MAY-1998; 98MO-CA00475.
XX
PR 10-OCT-1997; 97US-0061684.
XX
PR 15-MAY-1997; 97US-0046537.
XX
PA (LEVY); LEVY G.
XX
PI LeVY G;
XX
DR WP; 1995-059687/05.
XX
PT Modulating immune coagulation - by using Fgl2 antibodies and

PT compounds, used to treat conditions including graft rejection and foetal loss

PS Claim 4; Page 72; 105pp; English.

XX This peptide corresponds to amino acid residues 364-379 of human prothrombinase Fg12 (see AA08235). A claimed method of preventing or treating a condition requiring a reduction in immune coagulation comprises administering an inhibitor of Fg12. The inhibitor is preferably an antibody that binds to the Fg12 epitope. The condition to be treated in graft rejection of foetal loss (claimed).

XX Sequence 15 AA;
Query Match 100.0%; Score 88; DB 20; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.2e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DRYPSGNGCLYSSG 15
DB 1 DRYPSGNGCLYSSG 15
|||||

RESULT 2
AAE28619
ID AAE28619 standard; peptide; 14 AA.

AC AAE28619;

DT 27-DEC-2002 (first entry)

DE Human K+beta2 protein asparagine glycosylation site #1.

XX Human: potassium channel beta-subunit; K+beta2 protein; neural disorder; reproductive disorder; metabolic disorder; premature puberty; nephritis; endocrine disorder; memory disorder; neuroendocrine condition; asthma; spermatogenesis; renal disease; learning deficiency; Alzheimer's disease; neurodegenerative disease; proliferative disorder; autoimmune disease; carcinoma tumour; blood coagulation disease; blood platelet disease; rheumatoid arthritis; allergy; hyperproliferative disease; gene therapy; graft-versus-host disease; organ rejection; arteriosclerosis; thrombolytic; antiinflammatory; neuroprotective; anti-Parkinsonian; immunosuppressive; nephrotropic; cytostatic; nootropic; hypotensive; vulnary.

XX Homo sapiens.

XX WO200266601-A2.

XX 29-AUG-2002.

PF 24-JAN-2002; 2002WO-US02332.

XX 24-JAN-2001; 2001US-263872P.

PR 14-FEB-2001; 2001US-269794P.

XX (BRIM) BRISTOL-MYERS SQUIBB CO.

XX Feder J, Lee L, Chen J, Jackson D, Ramanathan C, Siemers N;

PI Chang H, Carroll P;

XX WPI; 2002-691617/74.

XX New potassium channel beta-subunit, K+beta2, proteins and nucleic acids, useful for diagnosing, treating and/or preventing e.g. reproductive, neural, metabolic, endocrine, memory, neurodegenerative disorders or diseases

PS Disclosure; Page 354; 366pp; English.

XX The present invention relates to human potassium channel beta-subunit (K+beta2) proteins and polynucleotides encoding such proteins. The K+beta2 sequences are useful for diagnosing, treating and/or preventing

CC reproductive disorders, neural disorders, disorders related to aberrant potassium regulation or hyper potassium channel activity, metabolic disorders (e.g. premature puberty), endocrine disorders (e.g. aberrant growth hormone synthesis and/or secretion), memory disorder, disorders of the testis (e.g. spermatogenesis), neuroendocrine condition related to aberrant thyroid hormone release, renal disease or disorders (e.g. nephritis), disorders related to aberrant higher brain function (e.g. learning deficiencies), neurodegenerative diseases (e.g. Alzheimer's disease), proliferative disorders (e.g. carcinoma tumour) and disorders involving excessive smooth muscle tone or excitability (e.g. asthma). They may be used to modulate haemostatic or thrombolytic activity, to treat or prevent blood coagulation diseases or disorders, blood platelet diseases, wounds, autoimmune diseases, disorders or conditions (e.g. rheumatoid arthritis), allergic reactions (e.g. asthma), organ rejection or graft-versus-host disease, and hyperproliferative diseases. K+beta2 sequences are also used in gene therapy. The present sequence is human K+beta2 protein asparagine glycosylation site.

XX Sequence 14 AA;

Query Match 42.0%; Score 37; DB 23; Length 14;

Best Local Similarity 75.0%; Pred. No. 57;

Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 5 SGNGCLY 12
DB 4 SGNGCRY 11
|||||

RESULT 3

AAU23853

ID AAU23853 standard; Peptide; 9 AA.

AC AAU23853;

DT 17-DEC-2001 (first entry)

DE Human MHC class I molecule HLA-A1 binding 103P2D6 peptide #38.

XX 103P2D6; PCR primer; DNA adaptor; prostate; testis; foetal tissue;

KW tumour; cancer; bone; ovary; breast; pancreas; colon; lung; cytostatic;

KW gene therapy; antibody therapy; ribosome; serum; blood; urine; bladder;

KW single chain monoclonal antibody; cervix; human.

XX Homo sapiens.

XX WO200162925-A2.

XX 30-AUG-2001.

PF 26-FEB-2001; 2001WO-US05996.

XX 24-FEB-2000; 2000US-0194558.

PR 13-JUL-2000; 2000US-0218856.

XX (UROC-) UROGENESYS INC.

XX Raitano AB, Afar DEH, Rastegar GS, Mitchell SC, Hubert AS;

PI Chailita-eld PM, Paris M, Jakobovits A;

XX WPI; 2001-557705/62.

XX New polynucleotide for treating and diagnosing prostate cancer is the

PT 103P2D6 gene which encodes for 103P2D6-related proteins

XX Example 15; Page 81; 132pp; English.

XX Sequences AAU23815-AAU24515 represent the 103P2D6-related protein and peptide fragments of the polypeptide. 103P2D6 is not expressed in normal adult tissue but is aberrantly expressed in some foetal tissues and many cancers including tumours of the prostate, testis, bladder, bone, cervix, ovary, breast, pancreas, colon and lung. The 103P2D6 polynucleotide, its related protein and also peptide fragments of the protein are therefore

CC useful for diagnosing and treating cancer. A vector comprising a
 CC polynucleotide which encodes a single chain monoclonal antibody, that
 CC immunospecifically binds to an 103P2D6-related protein, and a ribozyme
 CC capable of cleaving a polynucleotide having the 103P2D6 coding sequence,
 CC are both useful in the preparation of a composition for treating a
 CC patient with a cancer that expresses 103P2D6. The sequences can be used
 CC in diagnostic methods to monitor the level of 103P2D6 gene products in
 CC serum, blood, urine and tissue and to thereby detect the presence of
 CC cancerous cells.

XX
 XX
 SQ Sequence 9 AA;

Query Match 37.5%; Score 33; DB 22; Length 9;
 Best Local Similarity 75.0%; Pred. No. 9.3e+05;
 Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 5 SGNCGLYY 12
 : : | | | |
 DB 2 SGRGCLGY 9

RESULT 4
 AAU24319
 ID AAU24319 standard; Peptide; 9 AA.

XX
 XX
 AC AAU24319;
 XX
 DT 17-DEC-2001 (first entry)
 XX
 DE Human MHC class I molecule HLA-B7 binding 103P2D6 peptide #4.
 XX
 KW 103P2D6; PCR primer; DNA adaptor; prostate; testis; foetal tissue;
 KW tumour; cancer; bone; ovary; breast; pancreas; colon; lung; cytostatic;
 KW gene therapy; antibody therapy; ribozyme; serum; blood; urine; bladder;
 KW single chain monoclonal antibody; cervix; human.
 XX
 CS Homo sapiens.
 XX
 PN WC200162925-A2.
 PD 30-AUG-2001.
 XX
 PF 26-FEB-2000; 2001WO-US05996.
 XX
 PR 24-FEB-2000; 2000US-0184558.
 PR 13-JUL-2000; 2000US-0218856.
 XX
 PA (UROC-) UROGENESYS INC.
 XX
 PI Raitano AB, Afar DEH, Rastegar GS, Mitchell SC, Hubert RS;
 PI Challita-eid PM, Faris M, Jakobovits A;
 XX
 DR WPI; 2001-557705/62.
 XX
 PT New polynucleotide for treating and diagnosing prostate cancer is the
 PT 103P2D6 gene which encodes for 103P2D6-related proteins -
 XX
 PS Example 15; Page 94; 132pp; English.

XX
 CC Sequences AAU23815-AAU24515 represent the 103P2D6-related protein and
 CC peptide fragments of the polypeptide. 103P2D6 is not expressed in normal
 CC adult tissue but is aberrantly expressed in some foetal tissues and many
 CC cancers including tumours of the prostate, testis, bladder, bone, cervix,
 CC ovary, breast, pancreas, colon and lung. The 103P2D6 polynucleotide, its
 CC related protein and also peptide fragments of the protein are therefore
 CC useful for diagnosing and treating cancer. A vector comprising a
 CC polynucleotide which encodes a single chain monoclonal antibody, that
 CC immunospecifically binds to an 103P2D6-related protein, and a ribozyme
 CC capable of cleaving a polynucleotide having the 103P2D6 coding sequence,
 CC are both useful in the preparation of a composition for treating a
 CC patient with a cancer that expresses 103P2D6. The sequences can be used
 CC in diagnostic methods to monitor the level of 103P2D6 gene products in
 CC serum, blood, urine and tissue and to thereby detect the presence of
 CC cancerous cells.

CC cancerous cells.
 XX
 SQ Sequence 9 AA;

Query Match 37.5%; Score 33; DB 22; Length 9;
 Best Local Similarity 75.0%; Pred. No. 9.3e+05;
 Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 5 SGNCGLYY 12
 : : | | | |
 DB 1 SGRGCLGY a

RESULT 5
 AAU24423
 ID AAU24423 standard; Peptide; 9 AA.

XX
 AC AAU24423;
 XX
 DT 17-DEC-2001 (first entry)
 XX
 DE Human MHC molecule HLA-B35 binding 103P2D6 peptide #8.
 XX
 KW 103P2D6; PCR primer; DNA adaptor; prostate; testis; foetal tissue;
 KW tumour; cancer; bone; ovary; breast; pancreas; colon; lung; cytostatic;
 KW gene therapy; antibody therapy; ribozyme; serum; blood; urine; bladder;
 KW single chain monoclonal antibody; cervix; human.
 XX
 CS Homo sapiens.
 XX
 PN WC200162925-A2.
 PD 30-AUG-2001.
 XX
 PF 26-FEB-2000; 2001WO-US05996.
 XX
 PR 24-FEB-2000; 2000US-0184558.
 PR 13-JUL-2000; 2000US-0218856.
 XX
 PA (UROC-) UROGENESYS INC.
 XX
 PI Raitano AB, Afar DEH, Rastegar GS, Mitchell SC, Hubert RS;
 PI Challita-eid PM, Faris M, Jakobovits A;
 XX
 DR WPI; 2001-557705/62.
 XX
 PT New polynucleotide for treating and diagnosing prostate cancer is the
 PT 103P2D6 gene which encodes for 103P2D6-related proteins -
 XX
 PS Example 15; Page 97; 132pp; English.

XX
 CC Sequences AAU23815-AAU24515 represent the 103P2D6-related protein and
 CC peptide fragments of the polypeptide. 103P2D6 is not expressed in normal
 CC adult tissue but is aberrantly expressed in some foetal tissues and many
 CC cancers including tumours of the prostate, testis, bladder, bone, cervix,
 CC ovary, breast, pancreas, colon and lung. The 103P2D6 polynucleotide, its
 CC related protein and also peptide fragments of the protein are therefore
 CC useful for diagnosing and treating cancer. A vector comprising a
 CC polynucleotide which encodes a single chain monoclonal antibody, that
 CC immunospecifically binds to an 103P2D6-related protein, and a ribozyme
 CC capable of cleaving a polynucleotide having the 103P2D6 coding sequence,
 CC are both useful in the preparation of a composition for treating a
 CC patient with a cancer that expresses 103P2D6. The sequences can be used
 CC in diagnostic methods to monitor the level of 103P2D6 gene products in
 CC serum, blood, urine and tissue and to thereby detect the presence of
 CC cancerous cells.

XX
 SQ Sequence 9 AA;

Query Match 37.5%; Score 33; DB 22; Length 9;
 Best Local Similarity 75.0%; Pred. No. 9.3e+05;
 Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

```

CY 5 SGNCGLYY 12
  |||||
Db 2 SGRGGLGY 9

RESULT 6
AAU24441
ID AAU24441 standard; Peptide; 9 AA.
AC AAU24441;
XX
XX 17-DEC-2001 (first entry)
XX
XX Human MHC molecule HLA-B35 binding 103P2D6 peptide #26.
DE
XX 103P2D6; PCR primer; DNA adaptor; prostate; testis; foetal tissue.
XX tumour; cancer; bone; ovary; breast; pancreas; colon; lung; cytostatic;
XX gene therapy; antibody therapy; ribozyme; serum; blood; urine; bladder;
XX single chain monoclonal antibody; cervix; human.
XX
XX Homo sapiens.
XX
XX WO200162925-A2.
XX
XX 30-AUG-2001.
XX
XX 26-FEB-2001; 2001WO-US05996.
XX
XX 24-FEB-2000; 2000US-0184558.
XX
XX 13-JUL-2000; 2000US-0218856.
XX
XX (UROC-) UROGENESYS INC.
XX
XX Raitano AB, Afar DEH, Rastegar GS, Mitchell SC, Hubert RS;
XX Challita-eid PM, Paris M, Jakobovits A;
XX
XX WP1; 2001-557705/62.
XX
XX New polynucleotide for treating and diagnosing prostate cancer is the
XX 103P2D6 gene which encodes for 103P2D6-related proteins.
XX
XX Example 15; Page 98; 132pp; English.
XX
XX Sequences AAU23815-AAU24515 represent the 103P2D6-related protein and
XX peptide fragments of the polypeptide. 103P2D6 is not expressed in normal
XX adult tissue but is aberrantly expressed in some foetal tissues and many
XX cancers including tumours of the prostate, testis, bladder, bone, cervix,
XX ovary, breast, pancreas, colon and lung. The 103P2D6 polynucleotide, its
XX related protein and also peptide fragments of the protein are therefore
XX useful for diagnosing and treating cancer. A vector comprising a
XX polynucleotide which encodes a single chain monoclonal antibody, that
XX immunospecifically binds to an 103P2D6-related protein, and a ribozyme
XX capable of cleaving a polynucleotide having the 103P2D6 coding sequence,
XX are both useful in the preparation of a composition for treating a
XX patient with a cancer that expresses 103P2D6. The sequences can be used
XX in diagnostic methods to monitor the level of 103P2D6 gene products in
XX serum, blood, urine and tissue and to thereby detect the presence of
XX cancerous cells.
XX
XX Sequence 9 AA;
XX
XX Query Match 37.5%; Score 33; DB 22; Length 9;
XX Best Local Similarity 75.0%; Pred. No. 9.3e+05;
XX Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

CY 5 SGNCGLYY 12
  |||||
Db 1 SGRGGLGY 8

RESULT 7
AAU24484
ID AAU24484 standard; Peptide; 10 AA.

```

```

XX AAU24484;
XX
XX 17-DEC-2001 (first entry)
XX
XX Human MHC molecule HLA-A35 binding 103P2D6 peptide #19.
XX
XX 103P2D6; PCR primer; DNA adaptor; prostate; testis; foetal tissue;
XX tumour; cancer; bone; ovary; breast; pancreas; colon; lung; cytostatic;
XX gene therapy; antibody therapy; ribozyme; serum; blood; urine; bladder;
XX single chain monoclonal antibody; cervix; human.
XX
XX Homo sapiens.
XX
XX WC200162925-A2.
XX
XX 30-AUG-2001.
XX
XX 26-FEB-2001; 2001WO-US05996.
XX
XX 24-FEB-2000; 2000US-0184558.
XX
XX 13-JUL-2000; 2000US-0218856.
XX
XX (UROC-) UROGENESYS INC.
XX
XX Raitano AB, Afar DEH, Rastegar GS, Mitchell SC, Hubert RS;
XX Challita-eid PM, Paris M, Jakobovits A;
XX
XX WP1; 2001-557705/62.
XX
XX New polynucleotide for treating and diagnosing prostate cancer is the
XX 103P2D6 gene which encodes for 103P2D6-related proteins.
XX
XX Example 15; Page 99; 132pp; English.
XX
XX Sequences AAU23815-AAU24515 represent the 103P2D6-related protein and
XX peptide fragments of the polypeptide. 103P2D6 is not expressed in normal
XX adult tissue but is aberrantly expressed in some foetal tissues and many
XX cancers including tumours of the prostate, testis, bladder, bone, cervix,
XX ovary, breast, pancreas, colon and lung. The 103P2D6 polynucleotide, its
XX related protein and also peptide fragments of the protein are therefore
XX useful for diagnosing and treating cancer. A vector comprising a
XX polynucleotide which encodes a single chain monoclonal antibody, that
XX immunospecifically binds to an 103P2D6-related protein, and a ribozyme
XX capable of cleaving a polynucleotide having the 103P2D6 coding sequence,
XX are both useful in the preparation of a composition for treating a
XX patient with a cancer that expresses 103P2D6. The sequences can be used
XX in diagnostic methods to monitor the level of 103P2D6 gene products in
XX serum, blood, urine and tissue and to thereby detect the presence of
XX cancerous cells.
XX
XX Sequence 10 AA;
XX
XX Query Match 37.5%; Score 33; DB 22; Length 10;
XX Best Local Similarity 75.0%; Pred. No. 1.6e+02;
XX Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

CY 5 SGNCGLYY 12
  |||||
Db 2 SGRGGLGY 9

RESULT 8
AA826044
ID AA826044 standard; Peptide; 12 AA.
XX
XX AA826044;
XX
XX 05-JAN-2001 (first entry)
XX
XX Human IgE C-epsilon-2 PTHAb0011 peptide ligand SEQ ID NO:138.
XX
XX Epitope; mimotope; human; immunoglobulin E; IgE; C-epsilon-2 domain;
XX

```

KW allergic disease; immunoprophylaxis; immunotherapy; anti-allergic;
 KW immunosuppressive; vaccine; histamine release inhibitor; immunogen;
 KW allergy; atopy.

XX Homo sapiens.

XX WO200050460-A1.

PN 31-AUG-2000.

XX 22-FEB-2000; 2000WO-EP01455.

XX 25-FEB-1999; 99GB-0024405.

PR 29-MAR-1999; 99GB-0007151.

PR 07-MAY-1999; 99GB-0010537.

PR 07-MAY-1999; 99GB-0010538.

PR 07-AUG-1999; 99GB-0018594.

PR 07-AUG-1999; 99GB-0018603.

PR 07-SEP-1999; 99GB-0021046.

PR 07-SEP-1999; 99GB-0021047.

PR 29-OCT-1999; 99GB-0025619.

PR 23-NOV-1999; 99GB-0027695.

XX (SM'K) SMITHKLINE BEECHAM BIOLOGICALS.

PA (PEPT-) PEPTIDE THERAPEUTICS LTD.

XX Dyson M., Friede M., Greenwood J., Hewitt E., Lamont A., Mason S.

PI Randall R., Turnell WG., Van Vechelen MP., Vinals De Bassols YC.

XX WPI; 2000-572073/53.

XX Peptides useful for treating, preventing and ameliorating allergic

PT diseases, comprising an isolated surface exposed group of a specific

PT domain from immunoglobulin E -

XX Example 7; Page 53; 129pp; English.

XX The present invention describes a peptide (I) comprising an isolated

CC surface exposed group/epitope (II) of C-epsilon-2 domain (D) of

CC immunoglobulin E (IGE), or its mimotope. Also described are: (1) an

CC immunogen (II) for treating allergy comprising (I); (2) a vaccine (III)

CC for treating allergies comprising (II); (3) a ligand (IV) capable of

CC recognising E.; (4) a pharmaceutical composition (PC) comprising (IV);

CC (5) a peptide (Ia) capable of being recognised by (IV); (6) an immunogen

CC (Ia) comprising (Ia); and (7) producing (III) by producing (II). (I)

CC can have anti-allergic and immunosuppressive activities, and can be used

CC as a vaccine and histamine release inhibitor. (I), (II) and (III) are

CC useful in medicine and in the manufacture of medicaments for treating

CC and preventing allergies. (IV) is useful for identifying mimotopes of E,

CC in medicine and also in manufacturing medicaments for treating

CC allergies. (I) is useful in diagnostics and in the affinity purification

CC of circulating anti-IGE antibodies from blood. (I), (II) and (III) are

CC useful for treating a patient susceptible to or suffering from allergies.

CC (IV) is also useful in diagnosing atopy. AAB25907 to AAB26099 represent

CC peptide sequences which are used in the exemplification of the present

XX 07-NOV-2001 (first entry)

XX Peptide EED18/47/48 derived from Cepsilon2 region of human Ige.

XX Human; linkage technology; conjugated compound; carrier vehicle;

KW epitope; Cepsilon2; Cepsilon3; Cepsilon4; immunoglobulin E;

KW Ige mediated disease; antibody response.

XX Homo sapiens.

OS Synthetic.

XX WO200145745-A2.

XX 28-JUN-2001.

XX 21-DEC-2000; 2000WO-GB04935.

XX 21-DEC-1999; 99GB-0030233.

PR 22-FEB-2000; 2000GB-0004096.

PR 22-AUG-2000; 2000GB-0020707.

PR 22-AUG-2000; 2000GB-0020708.

XX (ACAM-) ACAMBIS RES LTD.

PA (SM'K) SMITHKLINE BEECHAM BIOLOGICALS.

XX Flinn N., Johnson T;

PI WPI; 2001-521967/57.

XX A linkage comprising an immunogenic conjugate useful treatment of Ige

PT mediated diseases -

XX Example 4; Page 23; 48pp; English.

XX The present invention relates to linkage methodology for use in the

CC conjugation of compounds (e.g. peptides) to carrier vehicles

CC (e.g. macromolecules, polymers, dendrimers, proteins) to produce a

CC biological and immunological constructs. The invention provides a

CC method for linking an epitope (e.g. a peptide) to a carrier (e.g. a

CC protein) for use in a pharmaceutical composition or a vaccine. The

CC invention describes peptides derived from or mimotopes of the

CC Cepsilon2, Cepsilon3 or Cepsilon4 regions of human immunoglobulin E

CC (IGE) which are used to produce conjugated compounds. The compounds or

CC compositions of the invention are useful in the manufacture of a

CC medicament for the treatment of IGE mediated diseases. The invention

CC allows for controlled conjugation of a peptide epitope (antigen) to a

CC protein so as to form an immunogenic conjugate which may be able to

CC raise a protective antibody response in an animal or human patient.

CC AAU16632-AAU16913 represent peptides derived from or mimotopes of

CC the Cepsilon2/Cepsilon3/Cepsilon4 region of human IGE.

XX Query Match 37.5%; Score 33; DB 22; Length 12;

Best Local Similarity 83.3%; Pred. No. 2e+02;

Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 4 PSNCG 9

DB 4 PSDCG 9

RESULT 10

AB000390

ID AB000390 standard; Peptide; 12 AA.

XX AC AB000390;

XX DT 02-SEP-2002 (first entry)

XX Human IGE cyclic immunogenic peptide SEQ ID NO: 174.

XX

KW Immunogen; human; IgE; immunoglobulin E; allergy; thio-ether linkage;
 KW vaccine; antiallergic; cyclic.
 XX Homo sapiens.
 CS WC200216409-A2.
 XX
 XX
 PD 28-FEB-2002.
 XX
 FF 17-AUG-2001; 2001WO-EF09576.
 XX
 PR 22-AUG-2000; 2000GB-0020717.
 XX
 XX (SMK) SMITHKLINE BEECHAM BIOLOGICALS.
 PA (PEPT-) PEPTIDE THERAPEUTICS LTD.
 XX
 PI Friede M, Mason S, Turneli WG, Vinal's Bassols YC;
 DR WPI; 2002-489648/52.
 XX
 XX Conjugate for use in vaccine for treatment of allergy, comprises
 PT disulfide bridge cyclized peptide and immunogenic carrier -
 XX
 XX Claim 4; Page 13; 45pp; English.
 PS
 CC The present invention relates to conjugates suitable for use in vaccines,
 CC where the conjugate comprises a disulfide bridge cyclised peptide and an
 CC immunogenic carrier. The vaccines can be used in the treatment of
 CC allergies. The present sequence is a cyclic peptide immunogen derived
 CC from human immunoglobulin E (IgE) suitable for use in the invention.
 XX
 XX Sequence 12 AA;
 SQ
 Query Match 37.5%; Score 33; DB 23; Length 12;
 Best Local Similarity 83.3%; Pred. No. 2e+02;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 4 PSCNCG 9
 DB
 PSCNCG 9
 PSCNCG 9
 RESULT 11
 AAW23509
 ID AAW23509 standard; peptide; 15 AA.
 XX
 AC AAW23509;
 XX
 DT 18-SEP-1997 (first entry)
 XX
 DE Purified cis-9,10-octadecenoamidase internal amino acid fragment.
 XX
 KW Coase; cis-9,10-octadecenoamide; oleic acid; catalysis;
 KW affinity chromatography; electric chromatography;
 KW gel filtration chromatography; ion exchange chromatography;
 KW partition chromatography; fatty acid primary amide; sleep-inducing;
 KW inhibitor; soporific; rat.
 XX
 OS Rattus rattus.
 XX
 PN WC9641869-A1.
 PD 27-DEC-1996.
 XX
 PF 12-JUN-1996; 96WO-US10435.
 XX
 XX 12-JUN-1995; 95US-0489535.
 XX (SCRI) SCRIPPS RES INST.
 PA
 XX Cravatt BF, Gilula NB, Lerner RA;
 XX WPI; 1997-065456/06.
 DR

XX Purified cis-9,10-octadecenoamidase - useful for hydrolysing
 PT sleep-inducing fatty acid primary amide(s), and identifying
 PT inhibitors
 XX
 PS Claim 1; Page 78; 101pp; English.
 XX
 CC A purified form of cis-9,10-octadecenoamidase (Coase) has been
 CC obtained by a chromatographic methodology selected from affinity,
 CC electric, gel filtration, ion exchange and partition chromatography.
 CC The Coase is characterised by enzymic activity for catalysing the
 CC conversion of cis-9,10-octadecenoamide (CO) to oleic acid and by the
 CC inclusion of an amino acid sequence fragment from rat liver Coase.
 CC The present sequence represents a specifically claimed example of such
 CC an amino acid fragment. This fragment is found at residues 31 to 45 of
 CC rat liver Coase as shown in AAW0465. The Coase can be used to catalyse
 CC the hydrolysis of fatty acid primary amides, which have sleep-inducing
 CC activity. The Coase can also be used to identify inhibitors of the
 CC Coase activity.
 XX
 SQ Sequence 15 AA;
 Query Match 37.5%; Score 33; DB 18; Length 15;
 Best Local Similarity 55.6%; Pred. No. 2.5e+02;
 Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
 QY 2 RYPSGNCGL 10
 DB RYPSGNCGL 10
 RYPSGNCGL 10
 RYPSGNCGL 10
 RESULT 12
 AAW57788
 ID AAW57788 standard; Peptide; 15 AA.
 XX
 AC AAW57788;
 XX
 DT 12-OCT-1998 (first entry)
 XX
 DE Fatty acid amide hydrolase peptide (e).
 XX
 KW Cis-9,10-octadecenoamidase; fatty acid amide hydrolase; FAAH;
 KW cleamide hydrolase; soporific; sleep.
 XX
 OS Mammalia.
 XX
 PN WC9820119-A1.
 XX
 PD 14-MAY-1998.
 XX
 PF 04-NOV-1997; 97WO-US20365.
 XX
 PR 04-NOV-1996; 96US-0743168.
 XX (SCRI) SCRIPPS RES INST.
 PA
 XX Cravatt BF, Gilula NB, Lerner RA;
 XX WPI; 1998-286935/25.
 XX
 XX New fatty acid amide hydrolase hydrolysing soporific unsaturated
 PT amide(s) - useful for, e.g. studying, and potentially developing
 PT agents for modulating sleep processes
 XX
 PS Claim 5; Page 111; 151pp; English.
 XX
 CC Fatty acid amide hydrolases (FAAHs) of the invention are
 CC characterised by inclusion of an amino acid sequence selected from
 CC a group of 28 sequences (see AAW57784-811). These FAAHs can hydrolyse
 CC cis-9,10-octadecenoamide, anandamide (arachidoyl ethanolamine), and
 CC myristic, palmitic or stearic amides. Also new are: (1) inhibiting
 CC hydrolysis of fatty acid primary amides catalysed by FAAH by
 CC treatment with an FAAH inhibitor; (2) a method of screening for an

CC FAAH inhibitor; (3) the FAAH inhibitor of formula
 CC CF3C(CH2)7-CH=CH(is)-(CH2)7Me; and (4) nucleic acid encoding FAAH
 CC or parts of it. FAAH catalyses conversion of fatty acid primary
 CC amides, particularly those in which the alkyl group has a cis
 CC unsaturation. These amides induce sleep, so FAAH can be used to
 CC study processes in which they are involved and also to develop
 CC agents for modulating sleep.

XX Sequence 15 AA;

Query Match 37.5%; Score 33; DB 19; Length 15;
 Best Local Similarity 55.6%; Pred. No. 2.5e+02;
 Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 2 RYPSGNCGL 10
 DB 1 RFPSAFPCI 9

RESULT 13

AAG96214
 ID AAG96214 standard; Peptide; 10 AA.

XX AC AAG96214;

XX DT 18-SEP-2001 (first entry)

DE Human complementary peptide, SEQ ID NO: 2408.

XX Human; complementary peptide; ligand; drug discovery; drug design.

OS Homo sapiens.

XX WO200142277-A2.

XX 14-JUN-2001.

XX 13-DEC-2000; 2000WC-GB04776.

XX 13-DEC-1999; 99GB-0029464.

XX (PROT-) PROTEOM LTD.

PI Roberts GW, Keai JR;

XX WPI; 2001-408419/43.

XX A set of peptide ligands consisting of specific complementary peptides
 PT to proteins encoded by genes of the human genome, useful in an assay
 PT for screening and identifying of one or more novel peptides which are
 PT drug candidates or pro-drugs.

FS Example 4; Page 386; 646pp; English.

XX The invention relates to a set of complementary peptide ligands
 CC generated from the human genome. The complementary peptides
 CC interact with their relevant target proteins encoded in the human
 CC genome. They can be used as reagents in drug discovery and as lead
 CC ligands to facilitate drug design and development. The present
 CC sequence is a complementary peptide provided in the specification.

XX Sequence 10 AA;

Query Match 35.2%; Score 31; DB 22; Length 10;
 Best Local Similarity 100.0%; Pred. No. 3.3e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 SGNCG 9

DB 6 SGNCG 10

RESULT 14

AAP40328
 ID AAP40328 standard; peptide; 15 AA.
 XX AAP40328;
 XX DT 16-AUG-2002 (updated)
 DT 30-JAN-1992 (first entry)
 XX Sequence of conotoxin peptide G1A.
 XX Acetylcholine receptor; reversible immobilisation;
 KW synaptic transmission inhibitor.
 XX Conus geographus.
 OS Synthetic.

XX Key Location/Qualifiers
 FT Disulfide-bond 2..7
 FT Modified-site 3

FT /label= Cys-S(acetamido-methyl)

FT Modified-site 13

FT /label= Cys-S(acetamido-methyl)

FT Modified-site 15

FT /label= Lys-NH2

XX US4447356-A.

XX 08-MAY-1984.

XX 04-JUN-1982; 82US-0385125.

XX 04-JUN-1982; 82US-0385125.

XX 17-APR-1981; 81US-0255237.

XX (OLIV/) OLIVERA B N.

XX Olivera RM, Cruz LC, Gray WR, Rivier JEP;

XX WPI; 1984-133757/21.

XX Conotoxin peptide(s) - useful for reversible immobilisation of
 PT muscles and for detecting acetylcholine receptors

XX Claim 5; column 2; 10pp; English.

XX The peptides of the invention are potent inhibitors of synaptic
 CC transmission at the neuromuscular junction while lacking inhibition
 CC of either nerve or muscle action potential propagation. Their action
 CC is freely reversible on dilution or removal of the peptides from the
 CC affected muscle. The peptides are useful for reversible
 CC immobilisation of a muscle or gp. of muscles in man and other
 CC vertebrates and they can be used for detection and measurement of
 CC acetylcholine receptors.
 CC (Updated on 16-AUG-2002 to add missing OS field.)

XX Sequence 15 AA;

Query Match 35.2%; Score 31; DB 5; Length 15;
 Best Local Similarity 62.5%; Pred. No. 4.9e+02;
 Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 8 CGLVYSSG 15

DB 7 CGRVYSCG 14

RESULT 15

AAR75265

ID AAR75265 standard; peptide; 15 AA.

XX AAR75265;

XX 21-DEC-1995 (first entry)

XX Alpha-conotoxin G1A peptide.
 DE
 XX Alpha conotoxin; inhibit; neuromuscular; synapse; signal transmission.
 XX
 OS Conus geographus.
 XX
 PN WO9511256-A1.
 XX
 XX 27-APR-1995.
 XX
 XX 19-OCT-1994; 94WO-US11927.
 PF
 XX 19-OCT-1993; 93US-0137900.
 PR
 XX (UTAH) UNIV UTAH RES FOUND.
 PA
 XX Cruz LJ, Hillyard DR, McIntosh JM, Olivera BM, Santos AD;
 PI WPI; 1995-170189/22.
 XX
 XX New A-lineage conotoxin peptide(s) - which inhibit synaptic
 PF transmission at the neuromuscular junction or are active against
 PR potassium or sodium channels
 XX
 XX Disclosure; Page 4; 66pp; English.
 XX
 CC The kappa-conotoxin, alpha conotoxin and alpha-like conotoxin
 CC peptides all belong to a group of peptides known as the A-lineage
 CC conotoxin peptides. The A lineage conotoxin peptides have a wide
 CC variety of pharmacological uses. The A-lineage conotoxin peptides
 CC claimed (AAK75264-R75293) are useful for the inhibition of synaptic
 CC transmission at neuromuscular junctions by blocking nicotinic acetylcholine
 CC receptors and they also have activity against voltage-gated Na
 CC and K channels.
 XX
 SQ Sequence 15 AA;

Query Match 35.2%; Score 31; DB 16; Length 15;
 Best Local Similarity 62.5%; Fred. No. 4.9e+02;
 Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 8 CGLYYSYG 15
 | | | | |
 Db 7 GGRHSCG 14

Search completed: November 5, 2003, 16:57:26
 Job time : 42 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

CM protein - protein search, using sw model

Run on: November 5, 2003, 16:58:41 / Search time 28 Seconds

(without alignments)
92.009 Million cell updates/sec

Title: US-09-902-563-18

Perfect score: 88

Sequence: 1 DRYPSGNGGLYSSG 15

Scoring table:

Gapop 10.0, Gapex: 0.5

Searched: 644079 seqs, 17:749292 residues

Total number of hits satisfying chosen parameters: 112152

Minimum DB seq length: 5

Maximum DB seq length: 15

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database: Published Applications AA:

- 1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOXB.pep:
- 2: /cgn2_6/ptodata/2/pubpaa/PTC1_NEW_PUB.pep:
- 3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep:
- 4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOXB.pep:
- 5: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep:
- 6: /cgn2_6/ptodata/2/pubpaa/PTCUS_PUBCOXB.pep:
- 7: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep:
- 8: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOXB.pep:
- 9: /cgn2_6/ptodata/2/pubpaa/US09_PUBCOXB.pep:
- 10: /cgn2_6/ptodata/2/pubpaa/US09B_PUBCOXB.pep:
- 11: /cgn2_6/ptodata/2/pubpaa/US09C_PUBCOXB.pep:
- 12: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep:
- 13: /cgn2_6/ptodata/2/pubpaa/US10A_PUBCOXB.pep:
- 14: /cgn2_6/ptodata/2/pubpaa/US10B_PUBCOXB.pep:
- 15: /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOXB.pep:
- 16: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep:
- 17: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep:
- 18: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOXB.pep:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	88	100.0	15	11	US-09-902-563-18
2	88	100.0	15	15	US-10-096-255-18
3	37	42.0	24	15	US-10-056-884-11
4	35	39.8	10	9	US-09-819-308-25
5	33	37.5	9	12	US-09-793-451-52
6	33	37.5	9	12	US-09-793-451-518
7	33	37.5	9	12	US-09-793-451-622
8	33	37.5	9	12	US-09-793-451-640
9	33	37.5	9	12	US-10-283-722-52
10	33	37.5	9	12	US-10-283-722-518
11	33	37.5	9	12	US-10-283-722-622
12	33	37.5	9	12	US-10-283-722-640
13	33	37.5	10	12	US-09-793-451-683
14	33	37.5	10	12	US-10-283-722-683
15	31	35.2	10	11	US-09-572-404B-240A

16	30	34.1	10	11	US-09-572-404B-490
17	30	34.1	12	12	US-10-218-906-20
18	30	34.1	14	12	US-10-125-187-16
19	30	34.1	14	12	US-10-125-187-17
20	30	34.1	14	12	US-10-125-187-50
21	30	34.1	14	12	US-10-125-187-51
22	29	33.0	10	12	US-09-793-451-572
23	29	33.0	10	12	US-09-793-451-677
24	29	33.0	10	12	US-10-283-722-677
25	29	33.0	10	12	US-10-283-722-677
26	28.5	32.4	10	7	US-08-344-824-254
27	28	31.8	6	15	US-10-131-543-3
28	28	31.8	6	15	US-10-131-546-3
29	28	31.8	6	15	US-10-131-546-3
30	28	31.8	11	11	US-09-924-993-6
31	28	31.8	15	15	US-10-161-493-55
32	27	30.7	7	11	US-09-792-286-22
33	27	30.7	7	11	US-09-792-286-225
34	27	30.7	9	9	US-09-832-723-80
35	27	30.7	9	12	US-10-303-331-80
36	27	30.7	10	11	US-09-572-404B-488
37	27	30.7	10	11	US-09-572-404B-3542
38	27	30.7	10	11	US-09-572-404B-3544
39	27	30.7	10	12	US-09-572-270A-581
40	27	30.7	11	11	US-09-852-910-48
41	27	30.7	14	11	US-09-924-993-7
42	27	30.7	14	12	US-10-125-187-18
43	27	30.7	14	12	US-10-125-187-52
44	27	30.7	14	15	US-10-219-834-97
45	27	30.7	15	14	US-10-086-623-25

ALIGNMENTS

RESULT 1
US-09-902-563-18
; Sequence 18, Application US/09902563
; Publication No. US20030059654A1
; GENERAL INFORMATION:
; APPLICANT: Levy, Gary
; TITLE OF INVENTION: Methods of Modulating Immune Coagulation
; FILE REFERENCE: 9579-17
; CURRENT APPLICATION NUMBER: US/09/902,563
; CURRENT FILING DATE: 2002-09-09
; PRIOR APPLICATION NUMBER: US 09/442,143
; PRIOR FILING DATE: 1999-11-15
; NUMBER OF SEQ ID NOS: 53
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 18
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-902-563-18

Query Match 100.0%; Score 88; DB 11; Length 15;
Best Local Similarity 100.0%; Pred No. 4.9e-07;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 DRYPSGNGGLYSSG 15
DB 1 DRYPSGNGGLYSSG 15
|||||

RESULT 2
US-10-096-255-18
; Sequence 18, Application US/10096255
; Publication No. US20030103974A1
; GENERAL INFORMATION:
; APPLICANT: Levy, Gary
; APPLICANT: Clark, David A.
; TITLE OF INVENTION: Methods of Modulating Immune Coagulation
; FILE REFERENCE: 9579-52

US-10-096-255-18

Query Match 100.0%; Score 82; DB 15; Length 15;
Best Local Similarity 100.0%; Pred. No. 4.9e-07;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DRYPSGNCGLYSSG 15
DB 1 DRYPSGNCGLYSSG 15

RESULT 3

US-10-056-884-11

Sequence 11; Application US/10056884
Publication No. US2003003788A1
GENERAL INFORMATION:
APPLICANT: Bristol-Myers Squibb Company
TITLE OF INVENTION: POLYNUCLEOTIDE ENCODING A NOVEL HUMAN POTASSIUM CHANNEL BETA-SUBUNIT
FILE REFERENCE: K-beta2
CURRENT APPLICATION NUMBER: US/10/056.884
CURRENT FILING DATE: 2002-01-24
PRIOR APPLICATION NUMBER: US 60/263,872
PRIOR FILING DATE: 2001-01-24
PRIOR APPLICATION NUMBER: US 60/269,794
PRIOR FILING DATE: 2001-02-14
NUMBER OF SEQ ID NOS: 73
SOFTWARE: PatentIn version 3.0
SEQ ID NO 11
LENGTH: 14
TYPE: PRT
ORGANISM: Homo sapiens

US-10-056-884-11

Query Match 100.0%; Score 82; DB 15; Length 15;
Best Local Similarity 100.0%; Pred. No. 4.9e-07;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DRYPSGNCGLYSSG 15
DB 1 DRYPSGNCGLYSSG 15

RESULT 5

US-09-793-451-52

Sequence 52; Application US/09793451
Publication No. US20030157597A1
GENERAL INFORMATION:
APPLICANT: Arthur B. Raitano
APPLICANT: Daniel E.H. Afar
APPLICANT: Gazelle S. Rastegar
APPLICANT: Steve Chappell Mitchell
APPLICANT: Rene S. Hubert
APPLICANT: Pia M. Chailita-Eid
APPLICANT: Mary Faris
APPLICANT: Aya Jakobovits
TITLE OF INVENTION: 103P2D6: TISSUE SPECIFIC PROTEIN HIGHLY EXPRESSED IN VARIOUS CANCERS
FILE REFERENCE: 129.20SU2
CURRENT APPLICATION NUMBER: US/09/793.451
CURRENT FILING DATE: 2001-02-26
PRIOR APPLICATION NUMBER: 60/184,558
PRIOR FILING DATE: 2000-02-24
PRIOR APPLICATION NUMBER: 60/218,856
PRIOR FILING DATE: 2000-07-13
NUMBER OF SEQ ID NOS: 752
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 52
LENGTH: 9
TYPE: PRT
ORGANISM: homo sapiens

US-09-793-451-52

Query Match 37.5%; Score 33; DB 12; Length 9;
Best Local Similarity 75.0%; Pred. No. 5.8e+05;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 5 SGNCGLY 12
DB 2 SGNCGLY 9

RESULT 6

US-09-793-451-518

Sequence 518; Application US/09793451
Publication No. US20030157597A1
GENERAL INFORMATION:
APPLICANT: Arthur B. Raitano
APPLICANT: Daniel E.H. Afar
APPLICANT: Gazelle S. Rastegar
APPLICANT: Steve Chappell Mitchell
APPLICANT: Rene S. Hubert
APPLICANT: Pia M. Chailita-Eid
APPLICANT: Mary Faris
APPLICANT: Aya Jakobovits
TITLE OF INVENTION: 103P2D6: TISSUE SPECIFIC PROTEIN HIGHLY EXPRESSED IN VARIOUS CANCERS
FILE REFERENCE: 129.20SU2
CURRENT APPLICATION NUMBER: US/09/793.451
CURRENT FILING DATE: 2001-02-26
PRIOR APPLICATION NUMBER: 60/184,558
PRIOR FILING DATE: 2000-02-24
PRIOR APPLICATION NUMBER: 60/218,856
PRIOR FILING DATE: 2000-07-13
NUMBER OF SEQ ID NOS: 752

Query Match 42.0%; Score 37; DB 15; Length 14;
Best Local Similarity 75.0%; Pred. No. 3.1;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 5 SGNCGLY 12
DB 4 SGNCRYY 11

RESULT 4

US-09-819-308-25

Sequence 25; Application US/09813308
Patent No. US20020019040A1
GENERAL INFORMATION:
APPLICANT: Daren-van Cotschot, Astrid
APPLICANT: Rohn, Jennifer
TITLE OF INVENTION: APOPTIN-ASSOCIATING PROTEIN
FILE REFERENCE: 2906-4820US
CURRENT APPLICATION NUMBER: US/09/819.308
CURRENT FILING DATE: 2001-03-27
NUMBER OF SEQ ID NOS: 46
SOFTWARE: PatentIn version 3.0
SEQ ID NO 25
LENGTH: 10
TYPE: PRT
ORGANISM: Sequence homology analysis of AAP-5

US-09-819-308-25

Query Match 39.8%; Score 35; DB 9; Length 10;
Best Local Similarity 85.7%; Pred. No. 46;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 8 CGLYSS 14
DB 3 CGLYSS 9

; SOFTWARE: FastSEQ for Windows Version 4.0

; SEQ ID NO 518

; LENGTH: 9

; TYPE: PRT

; ORGANISM: homo sapiens

US-09-793-451-518

Query Match 37.5%; Score 33; DB 12; Length 9;

Best Local Similarity 75.0%; Pred. No. 5.8e+05;

Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Cy 5 SGNCGLY 12

|||

Db 1 SGRCGLY 8

RESULT 7

US-09-793-451-622

; Sequence 622, Application US/09793451

; Publication No. US2003015797A1

; GENERAL INFORMATION:

; APPLICANT: Arthur B. Raitano

; APPLICANT: Daniel E.H. Afar

; APPLICANT: Gazelle S. Rastegar

; APPLICANT: Steve Chappell Mitchell

; APPLICANT: Rene S. Hubert

; APPLICANT: Pia M. Challita-Eid

; APPLICANT: Mary Paris

; APPLICANT: Aya Jakobovits

; TITLE OF INVENTION: 103P2D6: TISSUE SPECIFIC PROTEIN HIGHLY

; FILE REFERENCE: 129.2USU2 EXPRESSED IN VARIOUS CANCERS

; CURRENT APPLICATION NUMBER: US/09/793,451

; PRIOR FILING DATE: 2001-02-26

; PRIOR APPLICATION NUMBER: 60/184,558

; PRIOR FILING DATE: 2000-02-24

; PRIOR APPLICATION NUMBER: 60/218,856

; PRIOR FILING DATE: 2003-07-13

; NUMBER OF SEQ ID NOS: 752

; SOFTWARE: FastSEQ for Windows Version 4.0

; SEQ ID NO 622

; LENGTH: 9

; TYPE: PRT

; ORGANISM: homo sapiens

US-09-793-451-622

Query Match 37.5%; Score 33; DB 12; Length 9;

Best Local Similarity 75.0%; Pred. No. 5.8e+05;

Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Cy 5 SGNCGLY 12

|||

Db 2 SGRCGLY 9

RESULT 8

US-09-793-451-640

; Sequence 640, Application US/09793451

; Publication No. US2003015797A1

; GENERAL INFORMATION:

; APPLICANT: Arthur B. Raitano

; APPLICANT: Daniel E.H. Afar

; APPLICANT: Gazelle S. Rastegar

; APPLICANT: Steve Chappell Mitchell

; APPLICANT: Rene S. Hubert

; APPLICANT: Pia M. Challita-Eid

; APPLICANT: Mary Paris

; APPLICANT: Aya Jakobovits

; TITLE OF INVENTION: 103P2D6: TISSUE SPECIFIC PROTEIN HIGHLY

; FILE REFERENCE: 129.2USU2 EXPRESSED IN VARIOUS CANCERS

; CURRENT APPLICATION NUMBER: US/09/793,451

; PRIOR FILING DATE: 2001-02-26

; PRIOR APPLICATION NUMBER: 60/184,558

; PRIOR FILING DATE: 2000-02-24

; PRIOR APPLICATION NUMBER: 60/218,856

; PRIOR FILING DATE: 2000-07-13

; NUMBER OF SEQ ID NOS: 752

; SOFTWARE: FastSEQ for Windows Version 4.0

; SEQ ID NO 640

; LENGTH: 9

; TYPE: PRT

; ORGANISM: homo sapiens

US-09-793-451-640

Query Match 37.5%; Score 33; DB 12; Length 9;

Best Local Similarity 75.0%; Pred. No. 5.8e+05;

Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Cy 5 SGNCGLY 12

|||

Db 1 SGRCGLY 8

RESULT 9

US-10-283-722-52

; Sequence 52, Application US/10283722

; Publication No. US2003019407A1

; GENERAL INFORMATION:

; APPLICANT: Arthur B. Raitano

; APPLICANT: Daniel E.H. Afar

; APPLICANT: Gazelle S. Rastegar

; APPLICANT: Steve Chappell Mitchell

; APPLICANT: Rene S. Hubert

; APPLICANT: Pia M. Challita-Eid

; APPLICANT: Mary Paris

; APPLICANT: Aya Jakobovits

; TITLE OF INVENTION: 103P2D6: TISSUE SPECIFIC PROTEIN HIGHLY

; FILE REFERENCE: 129.2USU2 EXPRESSED IN VARIOUS CANCERS

; CURRENT APPLICATION NUMBER: US/10/283,722

; CURRENT FILING DATE: 2003-02-03

; PRIOR APPLICATION NUMBER: US/09/793,451

; PRIOR FILING DATE: 2001-02-26

; PRIOR APPLICATION NUMBER: 60/184,558

; PRIOR FILING DATE: 2000-02-24

; PRIOR APPLICATION NUMBER: 60/218,856

; PRIOR FILING DATE: 2000-07-13

; NUMBER OF SEQ ID NOS: 752

; SOFTWARE: FastSEQ for Windows Version 4.0

; SEQ ID NO 52

; LENGTH: 9

; TYPE: PRT

; ORGANISM: homo sapiens

US-10-283-722-52

Query Match 37.5%; Score 33; DB 12; Length 9;

Best Local Similarity 75.0%; Pred. No. 5.8e+05;

Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Cy 5 SGNCGLY 12

|||

Db 2 SGRCGLY 9

RESULT 10

US-10-283-722-518

; Sequence 518, Application US/10283722

; Publication No. US2003019407A1

; GENERAL INFORMATION:

; APPLICANT: Arthur B. Raitano

; APPLICANT: Daniel E.H. Afar

; APPLICANT: Gazelle S. Rastegar

; APPLICANT: Steve Chappell Mitchell

; APPLICANT: Rene S. Hubert

; APPLICANT: Pia M. Challita-Eid

```

; APPLICANT: Mary Faris
; APPLICANT: Ava Jakobovits
; TITLE OF INVENTION: 1032D6: TISSUE SPECIFIC PROTEIN HIGHLY
; FILE REFERENCE: 129.2USU2
; CURRENT APPLICATION NUMBER: US/09/793,451
; PRIOR FILING DATE: 2001-02-26
; PRIOR APPLICATION NUMBER: 60/184,558
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: 60/218,856
; NUMBER OF SEQ ID NOS: 752
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 518
; LENGTH: 9
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-283-722-518

```

```

Query Match      37.5%   Score 33;   DB 12;   Length 9;
Best Local Similarity 75.0%   Pred. No. 5.8e+05;
Matches 6;   Conservative 0;   Mismatches 2;   Indels 0;   Gaps 0;

```

```

QY  5  SGNCGLYY 12
DB  1  SGRCGLYG 8

```

```

RESULT 11
US-10-283-722-622
; Sequence 622, Application US/10283722
; Publication No. US20030194407A1
; GENERAL INFORMATION:
; APPLICANT: Arthur B. Raitano
; APPLICANT: Daniel E.H. Afar
; APPLICANT: Gazelle S. Rastegar
; APPLICANT: Steve Chappell Mitchell
; APPLICANT: Rene S. Hubert
; APPLICANT: Pia M. Challita-Eid
; APPLICANT: Mary Faris
; APPLICANT: Ava Jakobovits
; TITLE OF INVENTION: 1032D6: TISSUE SPECIFIC PROTEIN HIGHLY
; FILE REFERENCE: 129.2USU2
; CURRENT APPLICATION NUMBER: US/09/793,451
; PRIOR FILING DATE: 2001-02-26
; PRIOR APPLICATION NUMBER: 60/184,558
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: 60/218,856
; NUMBER OF SEQ ID NOS: 752
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 622
; LENGTH: 9
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-283-722-622

```

```

Query Match      37.5%   Score 33;   DB 12;   Length 9;
Best Local Similarity 75.0%   Pred. No. 5.8e+05;
Matches 6;   Conservative 0;   Mismatches 2;   Indels 0;   Gaps 0;

```

```

QY  5  SGNCGLYY 12
DB  2  SGRCGLYG 9

```

```

RESULT 12
US-10-283-722-640

```

```

; Sequence 640, Application US/10283722
; Publication No. US20030194407A1
; GENERAL INFORMATION:
; APPLICANT: Arthur B. Raitano
; APPLICANT: Daniel E.H. Afar
; APPLICANT: Gazelle S. Rastegar
; APPLICANT: Steve Chappell Mitchell
; APPLICANT: Rene S. Hubert
; APPLICANT: Pia M. Challita-Eid
; APPLICANT: Mary Faris
; APPLICANT: Ava Jakobovits
; TITLE OF INVENTION: 1032D6: TISSUE SPECIFIC PROTEIN HIGHLY
; FILE REFERENCE: 129.2USU2
; CURRENT APPLICATION NUMBER: US/10/283,722
; CURRENT FILING DATE: 2003-02-03
; PRIOR APPLICATION NUMBER: US/09/793,451
; PRIOR FILING DATE: 2001-02-26
; PRIOR APPLICATION NUMBER: 60/184,558
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: 60/218,856
; NUMBER OF SEQ ID NOS: 752
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 640
; LENGTH: 9
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-283-722-640

```

```

Query Match      37.5%   Score 33;   DB 12;   Length 9;
Best Local Similarity 75.0%   Pred. No. 5.8e+05;
Matches 6;   Conservative 0;   Mismatches 2;   Indels 0;   Gaps 0;

```

```

QY  5  SGNCGLYY 12
DB  1  SGRCGLYG 8

```

```

RESULT 13
US-09-793-451-683
; Sequence 683, Application US/09793451
; Publication No. US20030157597A1
; GENERAL INFORMATION:
; APPLICANT: Arthur B. Raitano
; APPLICANT: Daniel E.H. Afar
; APPLICANT: Gazelle S. Rastegar
; APPLICANT: Steve Chappell Mitchell
; APPLICANT: Rene S. Hubert
; APPLICANT: Pia M. Challita-Eid
; APPLICANT: Mary Faris
; APPLICANT: Ava Jakobovits
; TITLE OF INVENTION: 1032D6: TISSUE SPECIFIC PROTEIN HIGHLY
; FILE REFERENCE: 129.2USU2
; CURRENT APPLICATION NUMBER: US/09/793,451
; CURRENT FILING DATE: 2001-02-26
; PRIOR APPLICATION NUMBER: 60/184,558
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: 60/218,856
; PRIOR FILING DATE: 2000-07-13
; NUMBER OF SEQ ID NOS: 752
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 683
; LENGTH: 10
; TYPE: PRT
; ORGANISM: homo sapiens
US-09-793-451-683

```

```

Query Match      37.5%   Score 33;   DB 12;   Length 10;
Best Local Similarity 75.0%   Pred. No. 93;
Matches 6;   Conservative 0;   Mismatches 2;   Indels 0;   Gaps 0;

```

```
OY 5 SGNCGLY 12
Db 2 SGRGGLY 9

Search completed: November 5, 2003, 17:03:48
Job time : 28 secs

Db 6 SGNCG 10

RESULT 14
US-10-283-722-683
; Sequence 683, Application US/10283722
; Publication No. US20030194407A1
; GENERAL INFORMATION:
; APPLICANT: Arthur B. Raitano
; APPLICANT: Daniel E.H. Afar
; APPLICANT: Gazelle S. Rastegar
; APPLICANT: Steve Chappell Mitchell
; APPLICANT: Rene S. Hubert
; APPLICANT: Pia M. Chalitta-Eid
; APPLICANT: Mary Faris
; APPLICANT: Aya Jakobovits
; TITLE OF INVENTION: 103P256: TISSUE SPECIFIC PROTEIN HIGHLY
; FILE REFERENCE: 129, 2USU2
; CURRENT APPLICATION NUMBER: US/10/283,722
; PRIOR FILING DATE: 2003-02-03
; PRIOR APPLICATION NUMBER: US/09/793,451
; PRIOR FILING DATE: 2001-02-26
; PRIOR APPLICATION NUMBER: 60/184,558
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: 60/218,856
; PRIOR FILING DATE: 2000-07-13
; NUMBER OF SEQ ID NOS: 752
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 683
; LENGTH: 10
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-283-722-683

Query Match 37.5%; Score 33; DB 12; Length 10;
Best Local Similarity 75.0%; Pred. No. 93;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 5 SGNCGLY 12
Db 2 SGRGGLY 9

RESULT 15
US-09-572-404B-2408
; Sequence 2408, Application US/09572404B
; Publication No. US20030078374A1
; GENERAL INFORMATION:
; APPLICANT: Proteom Ltd
; TITLE OF INVENTION: Complementary peptide ligands from the human genome
; FILE REFERENCE: Human patent
; CURRENT APPLICATION NUMBER: US/09/572,404B
; CURRENT FILING DATE: 2000-05-17
; NUMBER OF SEQ ID NOS: 4203
; SOFTWARE: ProtPatent version 1.0
; SEQ ID NO 2408
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo Sapiens
; FEATURE:
; OTHER INFORMATION: sequence located in GATA1 OR GFI OR ERYF1 at 336-347 and may inte
; OTHER INFORMATION: with Sequence 2407 in this patent.
US-09-572-404B-2408

Query Match 35.2%; Score 31; DB 11; Length 10;
Best Local Similarity 100.0%; Pred. No. 1,98-02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 5 SGNCG 9
Db 11
```

GenCore version 5.1.6
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CM protein - protein search, using sw model

Run on: November 5, 2003, 16:56:41 ; Search time 22 Seconds
(without alignments)
28.848 Million cell updates/sec

Title: US-09-902-563-18

Perfect score: 88

Sequence: 1 DRYPSGNGGLYYSSG 15

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 328717 seqs, 42310358 residues

Total number of hits satisfying chosen parameters: 128097

Minimum DB seq length: 0

Maximum DB seq length: 15

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA:*

1: /cgn2_6/protdata/1/aa/5A_CCMB.pep:.*
2: /cgn2_6/protdata/1/aa/5B_CCMB.pep:.*
3: /cgn2_6/protdata/1/aa/6A_CCMB.pep:.*
4: /cgn2_6/protdata/1/aa/6B_CCMB.pep:.*
5: /cgn2_6/protdata/1/aa/9CTUS_COMB.pep:.*
6: /cgn2_6/protdata/1/aa/backfiles1.pep:.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Length	DB ID	Description
1	88	100.0	15	4 US-09-442-143A-18
2	33	37.5	15	3 US-08-743-168B-9
3	33	37.5	15	5 PCT-US96-10435-9
4	31	35.2	15	1 US-08-137-820-5
5	31	35.2	15	1 US-08-477-383-5
6	31	35.2	15	1 US-08-487-174-5
7	31	35.2	15	1 US-08-480-750-5
8	31	35.2	15	5 PCT-US96-07362-2
9	30	34.1	13	1 US-07-923-724-57
10	30	34.1	13	2 US-08-609-426A-57
11	30	34.1	13	2 US-08-374-652C-44
12	30	34.1	15	2 US-08-553-257A-42
13	30	34.1	15	4 US-09-441-992-42
14	29	33.0	15	2 US-08-432-871C-91
15	29	33.0	15	4 US-09-270-956-9
16	28.5	32.4	10	2 US-08-318-856A-72
17	28	31.8	7	4 US-08-492-411A-20
18	28	31.8	11	1 US-08-466-466-6
19	28	31.8	11	3 US-08-468-408-6
20	28	31.8	11	3 US-08-937-228-6
21	28	31.8	11	4 US-08-492-411A-33
22	28	31.8	11	4 US-08-421-583-6
23	28	31.8	11	4 US-09-639-242A-6
24	28	31.8	12	1 US-08-190-786A-2
25	28	31.8	12	1 US-08-383-474B-26
26	28	31.8	12	1 US-08-465-391A-2
27	28	31.8	12	2 US-08-464-538B-2

28 28 31.8 12 2 US-08-463-076B-65
29 28 31.8 12 3 US-08-737-841-13
30 28 31.8 13 1 US-08-089-994A-20
31 28 31.8 13 5 PCT-US94-07605-20
32 28 31.8 15 2 US-08-432-871C-100
33 28 31.8 15 4 US-09-347-504-55
34 28 31.8 15 4 US-09-270-956-100
35 27 30.7 13 3 US-08-881-037-88
36 27 30.7 14 1 US-08-466-468-7
37 27 30.7 14 3 US-08-468-408-7
38 27 30.7 14 3 US-08-937-228-7
39 27 30.7 14 4 US-08-421-583-7
40 27 30.7 14 4 US-08-639-242A-7
41 27 30.7 15 2 US-08-432-871C-80
42 27 30.7 15 2 US-08-432-871C-83
43 27 30.7 15 3 US-08-469-141A-14
44 27 30.7 15 4 US-09-347-504-68
45 27 30.7 15 4 US-09-347-504-74

ALIGNMENTS

RESULT 1
US-09-442-143A-18
; Sequence 18, Application US/09442143A
; Patent No. 6403C89
; GENERAL INFORMATION:
; APPLICANT: Levy, Gary
; TITLE OF INVENTION: Methods of Modulating Immune Coagulation
; FILE REFERENCE: 9579-14
; CURRENT APPLICATION NUMBER: US/09/442,143A
; PRIOR FILING DATE: 1999-11-15
; PRIOR APPLICATION NUMBER: US 60/646,537
; PRIOR FILING DATE: 1997-05-17
; PRIOR APPLICATION NUMBER: US 60/061,684
; PRIOR FILING DATE: 1997-10-10
; NUMBER OF SEQ ID NOS: 53
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 18
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-442-143A-18

Query Match 100.0%; Score 88; DB 4; Length 15;
Best Local Similarity 100.0%; Pred. No. 4.1e-07;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY : DRYPSGNGGLYYSSG 15
DB 1 DRYPSGNGGLYYSSG 15

RESULT 2
US-08-743-168B-9
; Sequence 9, Application US/087431699
; Patent No. 6271015
; GENERAL INFORMATION:
; APPLICANT: Gilula, No. 6271015ton B
; APPLICANT: Cravatt, Benjamin F
; APPLICANT: Lehrer, Richard A
; TITLE OF INVENTION: FATTY-ACID AMIDE HYDROLASE
; NUMBER OF SEQUENCES: 54
; CORRESPONDENCE ADDRESS:
ADDRESSEE: The Scripps Research Institute
STREET: 10550 No. 6271015th Torrey Pines Road
CITY: La Jolla
STATE: California
COUNTRY: US
ZIP: 92037
COMPUTER READABLE FORM:


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/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: PatentIn Release #1.0, Version #1.25
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/743.168B
/ FILING DATE: 04-NOV-1996
/ CLASSIFICATION: 435
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 08/489,535
/ FILING DATE: 12-JUN-1995
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Fitting, Thomas
/ REGISTRATION NUMBER: 34,163
/ REFERENCE/DOCKET NUMBER: TSR: 485.2
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (619) 784-2937
/ TELEFAX: (619) 784-9199
/ INFORMATION FOR SEQ ID NO: 9:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 15 amino acids
/ TYPE: amino acid
/ TOPOLOGY: linear
/ MOLECULE TYPE: Peptide
/ FRAGMENT TYPE: internal
/ US-08-743-168B-9

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```

Query Match          37.5%; Score 33; DB 3; Length 15;
Best Local Similarity 55.6%; Pred. No. 70;
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

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```

Qy 2 RYPSGNCGL 10
   |||||
Db 1 RPSAFCGI 9

```

```

RESULT 3
PCT-US96-10435-9
/ SEQUENCE 9, Application: PC/TUS9610435
/ GENERAL INFORMATION:
/ APPLICANT: The Scripps Research Institute
/ TITLE OF INVENTION: CIS-9, 10-OCTADECENOAMIDASE
/ NUMBER OF SEQUENCES: 32
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: PatentIn Release #1.0, Version #1.25
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: PCT/US96/10435
/ FILING DATE: 12-JUN-1996
/ CLASSIFICATION:
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 08/489,535
/ FILING DATE: 12-JUN-1995
/ INFORMATION FOR SEQ ID NO: 9:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 15 amino acids
/ TYPE: amino acid
/ TOPOLOGY: linear
/ MOLECULE TYPE: protein
/ FRAGMENT TYPE: internal
/ PCT-US96-10435-9

```

```

Query Match          37.5%; Score 33; DB 5; Length 15;
Best Local Similarity 55.6%; Pred. No. 70;
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

```

```

Qy 2 RYPSGNCGL 10
   |||||
Db 1 RPSAFCGI 9

```

```

RESULT 4
US-08-137-800-5
/ Sequence 5, Application US/08137800
/ Patent No. 55:4774
/ GENERAL INFORMATION:
/ APPLICANT: Olivera, Baldozero M.
/ APPLICANT: Cruz, Lourdes J.
/ APPLICANT: Hillyard, David R.
/ APPLICANT: McIntosh, J. Michael
/ APPLICANT: Santos, Ameurfin S.
/ TITLE OF INVENTION: Cocotoxin Peptides
/ NUMBER OF SEQUENCES: 53
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Venable, Baetjer, Howard & Civiletti
/ STREET: 1201 New York Avenue N.W., Suite 1000
/ CITY: Washington
/ STATE: DC
/ ZIP: 20005
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: Wordperfect 5.1
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/137,800
/ FILING DATE: 19-OCT-1993
/ CLASSIFICATION: 530
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Ihnen, Jeffrey J.
/ REGISTRATION NUMBER: 28,957
/ REFERENCE/DOCKET NUMBER: 24260-104763
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 202-962-4800
/ TELEFAX: 202-962-8300
/ INFORMATION FOR SEQ ID NO: 5:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 15 amino acids
/ TYPE: amino acid
/ TOPOLOGY: linear
/ MOLECULE TYPE: peptide
/ HYPOTHETICAL: NO
/ ANTI-SENSE: NO
/ ORIGINAL SOURCE:
/ ORGANISM: Conus geographus
/ US-08-137-800-5

```

```

Query Match          35.2%; Score 31; DB 1; Length 15;
Best Local Similarity 62.5%; Pred. No. 146+02;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

```

```

Qy 8 CGLYSSG 15
   |||||
Db 7 CCRHSCG 14

```

```

RESULT 5
US-08-477-383-5
/ Sequence 5, Application US/08477383
/ Patent No. 5589340
/ GENERAL INFORMATION:
/ APPLICANT: Olivera, Baldozero M.
/ APPLICANT: Cruz, Lourdes J.
/ APPLICANT: Hillyard, David R.
/ APPLICANT: Macintosh, J. Michael
/ APPLICANT: Santos, Ameurfin S.
/ TITLE OF INVENTION: Cocotoxin Peptides
/ NUMBER OF SEQUENCES: 59
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Venable, Baetjer, Howard & Civiletti
/ STREET: 1201 New York Avenue, N.W., Suite 1000
/ CITY: Washington
/ STATE: DC
/ COUNTRY: U.S.A.

```


TELEFAX: 202-962-8300
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
ORIGINAL SOURCE:
ORGANISM: *Corvus geographus*
US-08-480-750-5

Query Match 35.2% Score 31; DB 1; Length 15;
Best Local Similarity 62.5%; Pred. No. 1.4e+02;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 8 CGLYSSG 15
|||
DB 7 CGRYSCG 14

RESULT 8

PCT-US96-07962-2

Sequence 2, Application PC/TJS9607962
GENERAL INFORMATION:
APPLICANT: University of Utah Research Foundation
TITLE OF INVENTION: Use of Conotoxin Peptides U002 and W1
TITLE OF INVENTION: for Treating or Detecting Small-Cell Lung Carcinoma
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: Venable, Baetjer, Howard & Civiletti
STREET: 1201 New York Avenue, N.W., Suite 1000
CITY: Washington
STATE: DC
COUNTRY: U.S.A.
ZIP: 20005

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: MS-WINDOWS
SOFTWARE: Word 6.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US96/07962
FILING DATE: 04-JUN-1996
CLASSIFICATION:

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/487,174
FILING DATE: 07-JUN-1995
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-962-8300
TELEFAX: 202-962-8300
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
ORIGINAL SOURCE:
ORGANISM: *Corvus geographus*
PCT-US96-07962-2

Query Match 35.2% Score 31; DB 5; Length 15;
Best Local Similarity 62.5%; Pred. No. 1.4e+02;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 8 CGLYSSG 15
|||
DB 7 CGRYSCG 14

RESULT 9

US-07-923-724-57
Sequence 57, Application US/07923724
Patent No. 5780292
GENERAL INFORMATION:

APPLICANT: Nevalainen, Helena K.M.
APPLICANT: Paloheimo, Marja T.
APPLICANT: Miettinen-Oinonen, Arja S.K.
APPLICANT: Torkkeli, Tuula K.
APPLICANT: Cantrell, Michael
APPLICANT: Piddington, Christopher S.
APPLICANT: Rambossek, John A.
APPLICANT: Turunen, Marja K.
APPLICANT: Fagerström, Richard B.
TITLE OF INVENTION: Production of Phytase Degrading Enzymes
TITLE OF INVENTION: in Trichoderma
NUMBER OF SEQUENCES: 66
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sterne, Kessler, Goldstein & Fox
STREET: 1100 New York Avenue, Suite 600
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20005

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/923,724
FILING DATE: 31-JUL-1992
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/496,155
FILING DATE: 19-MAR-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/044,077
FILING DATE: 29-APR-1987
PRIOR APPLICATION DATA:
APPLICATION NUMBER: UK 8610600
FILING DATE: 30-APR-1986
ATTORNEY/AGENT INFORMATION:
NAME: Cimbala, Michele A.
REGISTRATION NUMBER: 33,851
REFERENCE/DOCKET NUMBER: 1850.024004
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 371-2600
TELEFAX: (202) 371-2540
INFORMATION FOR SEQ ID NO: 57:
SEQUENCE CHARACTERISTICS:
LENGTH: 13 amino acids
TYPE: amino acid
TOPOLOGY: both

US-07-923-724-57

Query Match 34.1% Score 30; DB 1; Length 13;
Best Local Similarity 55.6%; Pred. No. 1.7e+02;
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 DRYPSGNCG 9
:||||:
DB 4 EBYPSPSAG 12

RESULT 10

US-08-609-426A-57
Sequence 57, Application US/08609426A
Patent No. 5830733
GENERAL INFORMATION:

APPLICANT: Nevalainen, Helena K.M.
APPLICANT: Paloheimo, Marja T.
APPLICANT: Miettinen-Oinonen, Arja S.K.

```

; APPLICANT: Torkeli, Tuula K.
; APPLICANT: Cantrell, Michael
; APPLICANT: Piddington, Christopher S.
; APPLICANT: Rambosek, John A.
; APPLICANT: Turunen, Marja K.
; APPLICANT: Fagerström, Richard B.
; APPLICANT: Houston, Christine S.
; TITLE OF INVENTION: Production of Phytase Degrading Enzymes
; TITLE OF INVENTION: in Trichoderma
; NUMBER OF SEQUENCES: 69
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sterne, Kessler, Goldstein & Fox
; STREET: 1100 New York Avenue, Suite 602
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DCS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/609,426A
; FILING DATE: 01-MAR-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/923,724
; FILING DATE: 31-JUL-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/496,155
; FILING DATE: 19-MAR-1990
; PRIOR APPLICATION DATA: US 07/044,077
; FILING DATE: 29-APR-1987
; APPLICATION NUMBER: UK 8610500
; FILING DATE: 30-APR-1986
; ATTORNEY/AGENT INFORMATION:
; NAME: Reed, Grant E.
; REGISTRATION NUMBER: P-41,264
; REFERENCE/DOCKET NUMBER: 1050.0060C01
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 371-2600
; TELEFAX: (202) 371-2540
; INFORMATION FOR SEQ ID NO: 57:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 13 amino acids
; TYPE: amino acid
; TOPOLOGY: both
;
US-08-609-426A-57
Query Match 34.1%; Score 30; DB 2; Length 13;
Best Local Similarity 55.6%; Pred. No. 1.7e+02;
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 DRYPSGNCG 9
DB 4 ERYFSPSAG 12

RESULT 11
US-08-374-652C-44
; Sequence 44, Application US/08374652C
; Patent No. 5834286
; GENERAL INFORMATION:
; APPLICANT: NEVALAINEN, HELENA K.M.
; APPLICANT: PALOHEIMO, MARJA T.
; APPLICANT: FAGERSTRÖM, RICHARD B.
; APPLICANT: MIETTINEN-OINONEN, ARJA S.
; APPLICANT: TURUNEN, MARJA K.
; APPLICANT: RAMBOSEK, JOHN A.
; APPLICANT: PIDDINGTON, CHRISTOPHER S.

```

```

; APPLICANT: HOUSTON, CHRISTINE S.
; APPLICANT: CANTRELL, MICHAEL A.
; TITLE OF INVENTION: RECOMBINANT CELLS, DNA CONSTRUCTS,
; TITLE OF INVENTION: VECTORS AND METHODS FOR EXPRESSING PHYTASE DEGRADING
; TITLE OF INVENTION: ENZYMES IN DESIRED RATIOS
; NUMBER OF SEQUENCES: 94
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
; STREET: 1100 NEW YORK AVENUE, SUITE 600
; CITY: WASHINGTON
; STATE: DC
; COUNTRY: USA
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DCS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/374,652C
; FILING DATE: 24-MAY-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US93/07058
; FILING DATE: 27-JUL-1993
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/925,401
; FILING DATE: 31-JUL-1992
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: REED, GRANT E.
; REGISTRATION NUMBER: 41,264
; REFERENCE/DOCKET NUMBER: 1050.071001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-2600
; TELEFAX: 202-371-2540
; INFORMATION FOR SEQ ID NO: 44:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 13 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: not relevant
; MOLECULE TYPE: peptide
;
US-08-374-652C-44
Query Match 34.1%; Score 30; DB 2; Length 13;
Best Local Similarity 55.6%; Pred. No. 1.7e+02;
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 DRYPSGNCG 9
DB 4 ERYFSPSAG 12

RESULT 12
US-08-553-257A-42
; Sequence 42, Application US/08553257A
; Patent No. 594083
; GENERAL INFORMATION:
; APPLICANT: ISTITUTO DI RICERCHE DI BIOLOGIA
; APPLICANT: MOLECOLARE P. ANGELETTI S.p.A.
; APPLICANT: FELICI, Franco
; APPLICANT: LUZZAGO, Alessandra
; APPLICANT: NICOSIA, Alfredo
; APPLICANT: MONACI, Paolo
; APPLICANT: CORTESE, Riccardo
; TITLE OF INVENTION: PROCESS FOR THE PREPARATION OF IMMUNOGENS
; TITLE OF INVENTION: OR DIAGNOSTIC REAGENTS, AND IMMUNOGENS OR
; TITLE OF INVENTION: DIAGNOSTIC REAGENTS THEREBY OBTAINABLE
; NUMBER OF SEQUENCES: 68
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Browdy and Neimark

```

```

/ STREET: 419 Seventh Street N.W. Ste. 300
/ CITY: Washington
/ STATE: D.C.
/ COUNTRY: USA
/ ZIP: 20004
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: Patent in Release #1.0, Version #1.30
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/553.257A
/ FILING DATE:
/ CLASSIFICATION: 435
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: PCT/IT94/00054
/ FILING DATE: 05-MAY-1994
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: RM93A003301
/ FILING DATE: 11-MAY-1993
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Browdy, Roger L.
/ REGISTRATION NUMBER: 25,618
/ REFERENCE/DOCKET NUMBER: FELICI=1
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (202) 628-5197
/ TELEFAX: (202) 737-3528
/ INFORMATION FOR SEQ ID NO: 42:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 15 amino acids
/ TYPE: amino acid
/ STRANDEDNESS: linear
/ TOPOLOGY: linear
/ MOLECULE TYPE: recombinant protein
/ HYPOTHETICAL: yes
/ FRAGMENT TYPE: internal
/ IMMEDIATE SOURCE:
/ LIBRARY: of recombinant peptides on phage
/ CLONE: phagic
/ FEATURE:
/ NAME/KEY: polypeptide
/ IDENTIFICATION METHOD: selection with specific antibodies
/ US-09-553-257A-42
/
/ Query Match 34.1%; Score 30; DB 2; Length 15;
/ Best Local Similarity 83.3%; Pred. No. 2e+02;
/ Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
/
/ QY 4 PSGNCG 9
/ Db 9 PSGACG 14
/
/ RESULT 13
/ US-09-441-992-42
/ Sequence 42, Application US/09441992
/ Patent No. 6541210
/ GENERAL INFORMATION:
/ APPLICANT: ISTITUTO DI RICERCA DI BIOLOGIA
/ MOLECULAR P. ANGELINI S.P.A.
/ FELICI, Franco
/ LUZZAGO, Alessandra
/ NICOSIA, Alfredo
/ MONACI, Paolo
/ CORTESE, Riccardo
/ TITLE OF INVENTION: PROCESS FOR THE PREPARATION OF IMMUNOGENS
/ OR DIAGNOSTIC REAGENTS, AND IMMUNOGENS OR
/ DIAGNOSTIC REAGENTS THEREBY OBTAINABLE
/
/ NUMBER OF SEQUENCES: 68
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Browdy and Neimark
/ STREET: 419 Seventh Street N.W. Ste. 300
/ CITY: Washington

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/ STATE: D.C.
/ COUNTRY: USA
/ ZIP: 20004
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: Patent in Release #1.0, Version #1.30
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/09/441.992
/ FILING DATE: 16-No. 654-210-1999
/ CLASSIFICATION: <Unknown>
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: 08/553.257
/ FILING DATE: <Unknown>
/ APPLICATION NUMBER: RM93A003301
/ FILING DATE: 11-MAY-1993
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Browdy, Roger L.
/ REGISTRATION NUMBER: 25,618
/ REFERENCE/DOCKET NUMBER: FELICI=1
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (202) 628-5197
/ TELEFAX: (202) 737-3528
/ INFORMATION FOR SEQ ID NO: 42:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 15 amino acids
/ TYPE: amino acid
/ STRANDEDNESS: linear
/ TOPOLOGY: linear
/ MOLECULE TYPE: recombinant protein
/ HYPOTHETICAL: yes
/ FRAGMENT TYPE: internal
/ IMMEDIATE SOURCE:
/ LIBRARY: of recombinant peptides on phage
/ CLONE: phagic
/ FEATURE:
/ NAME: polypeptide
/ (ix)
/ SEQUENCE DESCRIPTION: SEQ ID NO: 42:
/ US-09-441-992-42
/
/ Query Match 34.1%; Score 30; DB 4; Length 15;
/ Best Local Similarity 83.3%; Pred. No. 2e+02;
/ Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
/
/ QY 4 PSGNCG 9
/ Db 9 PSGACG 14
/
/ RESULT 14
/ US-08-432-871C-91
/ Sequence 91, Application US/08432871C
/ Patent No. 5877610
/ GENERAL INFORMATION:
/ APPLICANT: Loeb, Lawrence A.
/ APPLICANT: Black, Margaret E.
/ TITLE OF INVENTION: THYMIDINE KINASE MUTANTS
/ NUMBER OF SEQUENCES: 104
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Seed and Berry LLP
/ STREET: 6300 Columbia Center, 701 Fifth Avenue
/ CITY: Seattle
/ STATE: Washington
/ COUNTRY: US
/ ZIP: 98104-7092
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: Patent in Release #1.0, Version #1.25
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/432.871C

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SEARCH COMPLETED: November 5, 2003, 16:59:42
Job time : 22 secs

FILED DATE: 02-MAY-1995
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: McMasters, David D.
REGISTRATION NUMBER: 33,963
REFERENCE/DOCKET NUMBER: 240052.409C1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
TELEX: 3723836
INFORMATION FOR SEQ ID NO: 91:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 amino acids
TYPE: amino acid
TOPOLOGY: linear
US-08-432-871C-91

Query Match 33.0%; Score 29; DB 2; Length 15;
Best Local Similarity 45.5%; Pred. No. 2.8e+02;
Matches 5; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 1 DRYPSGNCGLY 11
DB 4 DRHPIGQTSY 14

RESULT 15
US-09-270-956-91
Sequence 91, Application US/09270956
Patent No. 6451571
GENERAL INFORMATION:
APPLICANT: Loeb, Lawrence A.
APPLICANT: Black, Margaret E.
TITLE OF INVENTION: THYMIDINE KINASE MUTANTS
NUMBER OF SEQUENCES: 104
CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED and BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
CITY: Seattle
STATE: Washington
COUNTRY: US
ZIP: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/270,956
FILING DATE: 17-MAR-1999
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: McMasters, David D.
REGISTRATION NUMBER: 33,963
REFERENCE/DOCKET NUMBER: 240052.409C3
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
TELEX: 3723836
INFORMATION FOR SEQ ID NO: 91:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 amino acids
TYPE: amino acid
TOPOLOGY: linear
US-09-270-956-91

Query Match 33.0%; Score 29; DB 4; Length 15;
Best Local Similarity 45.5%; Pred. No. 2.8e+02;
Matches 5; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 1 DRYPSGNCGLY 11
DB 4 DRHPIGQTSY 14